

## SEQUENCE LISTING

<110> Duvick, Jonathan P.  
 Gilliam, Jacob T.  
 Maddox, Joyce R.  
 Rao, Aragula Gururaj  
 Crasta, Oswald R.  
 Folkerts, Otto

<120> Amino Polyol Amine Oxidase  
 Polynucleotides and Related Polypeptides and Methods of Use

<130> 1134R

<150> US 60/092,936

<151> 1998-07-25

<150> US 60/135,392

<151> 1999-05-21

<150> US 09/352,159

<151> 1999-07-12

<150> US 09/352,168

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<160> 53

<170> FastSEQ for Windows Version 3.0

<210> 1

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<212> DNA

<213> *Exophiala spinifera*

<220>

<221> misc\_feature

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attgtcgatc gacgtcgatg ctggtatctc tggcaaatga gatgggggtca cagctcgatt	180
ggaggacgcc cgagaagcct tgttcgcgcc accacggcct gtcccatatc aagactatct	240
tgctatagta gccacaggata gaattttccg ccaatgcttg cttctcggcg ggaagaggtg	300
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ggaacacggc gc	372

<210> 2

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<213> *Exophiala spinifera*

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 gatcgtagtg tacagccgga tgcgactgc tcaatttcag ccacgggggt gttgaggtgc 180  
 ac 182

<210> 3  
 <211> 29  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Designed oligonucleotide for 3' RACE, N21965

<400> 3  
 tgggttcggt accgacaacc ttgtatccc 29

<210> 4  
 <211> 28  
 <212> DNA  
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<220>  
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<210> 5  
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 <213> *Exophiala spinifera*

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 <222> (1)...(1386)

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 1 5 10 15

gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctg gtc ctt 96  
 Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu  
 20 25 30

gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc ggt 144  
 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45

ccc ggc agg acg act atc aac gac ctg ggc gct gcg tgg atc aat gac 192  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60

agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag 240  
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80

ggc gag ctg cag agg acg act gga aat tca atc cat caa gca caa gac 288

Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp		
				85					90						95		
ggt	aca	acc	act	aca	gct	cct	tat	ggt	gac	ccc	ttg	ctg	agc	gag	gag	336	
Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu		
			100					105					110				
ggt	gca	agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	384	
Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile		
			115				120					125					
gaa	gag	cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	egg	432	
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
		130				135					140						
ctc	gac	agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	480	
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150				155					160			
cct	gct	gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	ggc	gct	ctg	ctc	ggt	528	
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
			165					170					175				
gtg	gaa	goc	cac	gag	atc	agc	atg	ctt	ttt	ctc	acc	gac	tac	atc	aag	576	
Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185					190				
agt	gcc	acc	ggt	ctc	agt	aat	att	tcc	tcg	gac	aag	aaa	gac	ggc	ggg	624	
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
		195				200						205					
cag	tat	atg	cga	tgc	aaa	aca	ggt	atg	cag	tcg	att	tgc	cat	gcc	atg	672	
Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
	210					215					220						
tca	aag	gaa	ctt	gtt	cca	ggc	tca	gtg	cac	ctc	aac	acc	ccc	gtc	gct	720	
Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225				230						235				240			
gaa	att	gag	cag	tcg	gca	ccc	ggc	tgt	aca	gta	cga	tcg	gcc	tcg	ggc	768	
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
			245					250					255				
gcc	gtg	tcc	cga	agc	aaa	aag	gtg	gtg	gtt	tcg	tta	ccg	aca	acc	ttg	816	
Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265					270				
tat	ccc	acc	ttg	aca	ttt	tca	cca	cct	ctt	ccc	gcc	gag	aag	caa	gca	864	
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
		275					280					285					
ttg	gcg	gaa	aat	tct	atc	ctg	ggc	tac	tat	agc	aag	ata	gtc	ttc	gta	912	
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
		290					295				300						
tcg	gac	aag	ccg	tcg	tcg	cgc	gaa	caa	ggc	tcc	tcg	ggc	gtc	ctc	caa	960	
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
305					310				315					320			

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tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc      1008
Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val
          325                      330                      335

gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg      1056
Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg
          340                      345                      350

aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac      1104
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
          355                      360                      365

caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg      1152
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
          370                      375                      380

gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa gga      1200
Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
          385                      390                      395                      400

gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgg      1248
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
          405                      410                      415

ccg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg      1296
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
          420                      425                      430

tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa      1344
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
          435                      440                      445

cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca      1386
Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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tag      1389

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<210> 6
<211> 462
<212> PRT
<213> Exophiala spinifera

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Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
 35      40      45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
 50      55      60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
 65      70      75      80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
 85      90      95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
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Val	Ala	Ser	100	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	110	Gln	Leu	Ile
			115					120						125			
Glu	Glu	His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg		
			130					135					140				
Leu	Asp	Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu		
145					150					155					160		
Pro	Ala	Val	Leu	Gly	Val	Ala	Asn	Gln	Ile	Thr	Arg	Ala	Leu	Leu	Gly		
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Val	Glu	Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys		
			180					185						190			
Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly		
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Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly	Met	Gln	Ser	Ile	Cys	His	Ala	Met		
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Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser	Val	His	Leu	Asn	Thr	Pro	Val	Ala		
225					230						235				240		
Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly	Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly		
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Ala	Val	Phe	Arg	Ser	Lys	Lys	Val	Val	Val	Ser	Leu	Pro	Thr	Thr	Leu		
			260					265						270			
Tyr	Pro	Thr	Leu	Thr	Phe	Ser	Pro	Pro	Leu	Pro	Ala	Glu	Lys	Gln	Ala		
			275				280						285				
Leu	Ala	Glu	Asn	Ser	Ile	Leu	Gly	Tyr	Tyr	Ser	Lys	Ile	Val	Phe	Val		
			290				295				300						
Trp	Asp	Lys	Pro	Trp	Trp	Arg	Glu	Gln	Gly	Phe	Ser	Gly	Val	Leu	Gln		
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Ser	Ser	Cys	Asp	Pro	Ile	Ser	Phe	Ala	Arg	Asp	Thr	Ser	Ile	Asp	Val		
				325					330					335			
Asp	Arg	Gln	Trp	Ser	Ile	Thr	Cys	Phe	Met	Val	Gly	Asp	Pro	Gly	Arg		
			340					345					350				
Lys	Trp	Ser	Gln	Gln	Ser	Lys	Gln	Val	Arg	Gln	Lys	Ser	Val	Trp	Asp		
			355				360					365					
Gln	Leu	Arg	Ala	Ala	Tyr	Glu	Asn	Ala	Gly	Ala	Gln	Val	Pro	Glu	Pro		
			370				375				380						
Ala	Asn	Val	Leu	Glu	Ile	Glu	Trp	Ser	Lys	Gln	Gln	Tyr	Phe	Gln	Gly		
385					390					395					400		
Ala	Pro	Ser	Ala	Val	Tyr	Gly	Leu	Asn	Asp	Leu	Ile	Thr	Leu	Gly	Ser		
				405				410						415			
Ala	Leu	Arg	Thr	Pro	Phe	Lys	Ser	Val	His	Phe	Val	Gly	Thr	Glu	Thr		
			420					425					430				
Ser	Leu	Val	Trp	Lys	Gly	Tyr	Met	Glu	Gly	Ala	Ile	Arg	Ser	Gly	Gln		
			435				440					445					
Arg	Gly	Ala	Ala	Glu	Val	Val	Ala	Ser	Leu	Val	Pro	Ala	Ala				
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&lt;210&gt; 7

&lt;211&gt; 1442

&lt;212&gt; DNA

&lt;213&gt; Exophiala spinifera

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(646)

&lt;221&gt; intron

&lt;222&gt; (647)...(699)

&lt;221&gt; CDS

&lt;222&gt; (700) ... (1439)

&lt;400&gt; 7

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gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt	96
Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu	
20 25 30	
gag ggc atg gat cgt gta ggg gga aag act ctg agc gta caa tgc ggt	144
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly	
35 40 45	
ccc ggc agg acg act atc aac gac ctc ggc gct ggc tgg atc aat gac	192
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp	
50 55 60	
agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag	240
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu	
65 70 75 80	
ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa gac	288
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp	
85 90 95	
ggg aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag gag	336
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu	
100 105 110	
gtt gca agt gca ctt ggc gaa ctc ctc ccc gta tgg tct cag ctg atc	384
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile	
115 120 125	
gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag ggc aag cgg	432
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg	
130 135 140	
ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac ttg	480
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu	
145 150 155 160	
cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc ggt	528
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly	
165 170 175	
gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc aag	576
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys	
180 185 190	
agt gcc acc ggt ctc agt aat att ttc tgc gac aag aaa gac ggc ggg	624
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly	
195 200 205	
cag tat gtg cga tgc aaa aca g' gtgcgtgtgg' tgcgcgcaca ggtgggggac	676
Gln Tyr Val Arg Cys Lys Thr	

210	215	
tcgtttctca gtgggtcattc cag gt atg cag tcg att tgc cat gcc atg tca		728
	Gly Met Gln Ser Ile Cys His Ala Met Ser	
	220 225	
aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa		776
Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu		
	230 235 240	
att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc		824
Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala		
	245 250 255	
gtg ttc cga agc aaa aag gag gtg gtt tcg tta ccg aca acc ttg tat		872
Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr		
	260 265 270	
ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg		920
Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu		
	275 280 285	
gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg		968
Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp		
	290 295 300 305	
gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg		1016
Asp Lys Pro Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser		
	310 315 320	
agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat		1064
Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp		
	325 330 335	
cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag		1112
Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys		
	340 345 350	
tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa		1160
Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln		
	355 360 365	
ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc		1208
Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala		
	370 375 380 385	
aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa gga gct		1256
Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala		
	390 395 400	
ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt tcg gcg		1304
Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala		
	405 410 415	
ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct		1352
Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser		
	420 425 430	

tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgg ggt caa cga 1400  
 Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg  
 435 440 445

ggg gct gca gaa gtc gtg gct agc ctg gtg cca gca gca tag 1442  
 Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

<210> 8  
 <211> 462  
 <212> PRT  
 <213> *Exophiala spinifera*

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 Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly  
 35 40 45  
 Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp  
 50 55 60  
 Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu  
 65 70 75 80  
 Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Cln Ala Gln Asp  
 85 90 95  
 Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu  
 100 105 110  
 Val Ala Ser Ala Leu Ala Glu Leu Pro Val Trp Ser Gln Leu Ile  
 115 120 125  
 Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg  
 130 135 140  
 Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu  
 145 150 155 160  
 Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly  
 165 170 175  
 Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys  
 180 185 190  
 Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly  
 195 200 205  
 Gln Tyr Val Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met  
 210 215 220  
 Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala  
 225 230 235 240  
 Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly  
 245 250 255  
 Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu  
 260 265 270  
 Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala  
 275 280 285  
 Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val  
 290 295 300  
 Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln  
 305 310 315 320  
 Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val  
 325 330 335  
 Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg



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          340          345          350
Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp
          355          360          365
Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro
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Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly
          385          390          395          400
Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser
          405          410          415
Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr
          420          425          430
Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln
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Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
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<210> 9
<211> 458
<212> PRT
<213> Exophiala spinifera

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20     25     30
Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly
35     40     45
Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp
50     55     60
Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu
65     70     75     80
Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp
85     90     95
Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu
100    105    110
Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile
115    120    125
Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg
130    135    140
Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu
145    150    155    160
Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly
165    170    175
Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys
180    185    190
Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly
195    200    205
Gln Tyr Val Arg Cys Lys Thr Gly Ala Cys Gly Val Val Ser Gly Gly
210    215    220
Gly Leu Val Ser Gln Trp Ser Phe Gln Val Cys Ser Arg Phe Ala Met
225    230    235    240
Pro Cys Gln Arg Asn Leu Phe Gln Ala Gln Cys Thr Ser Thr Pro Pro
245    250    255
Ser Leu Lys Leu Ser Ser Arg His Pro Ala Val Gln Tyr Asp Arg Pro
260    265    270
Arg Ala Pro Cys Ser Glu Ala Lys Arg Trp Trp Phe Arg Tyr Arg Gln
275    280    285

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Pro Cys Ile Pro Pro His Phe His His Leu Phe Pro Pro Arg Ser Lys
290                295                300
His Trp Arg Lys Ile Leu Ser Trp Ala Thr Ile Ala Arg Ser Ser Tyr
305                310                315                320
Gly Thr Ser Arg Gly Gly Ala Asn Lys Ala Ser Arg Ala Ser Ser Asn
                325                330                335
Arg Ala Val Thr Pro Ser His Leu Pro Glu Ile Pro Ala Ser Thr Ser
                340                345                350
Ile Asp Asn Gly Pro Leu Pro Val Ser Trp Ser Glu Thr Arg Asp Gly
                355                360                365
Ser Gly Pro Asn Ser Pro Ser Arg Tyr Asp Lys Ser Leu Ser Gly Thr
                370                375                380
Asn Ser Ala Gln Pro Thr Arg Thr Pro Gly Pro Lys Ser Gln Ser Arg
385                390                395                400
Pro Thr Cys Ser Lys Ser Ser Gly Arg Ser Ser Ser Ile Ser Lys Glu
                405                410                425
Leu Arg Ala Pro Ser Met Gly Thr Ile Ser Ser His Trp Val Arg Arg
                420                425                430
Ser Glu Arg Arg Ser Arg Val Phe Ile Ser Leu Glu Arg Arg Arg Leu
                435                440                445
Phe Gly Lys Gly Ile Trp Lys Gly Pro Tyr
450                455

```

```

<210> 10
<211> 1392
<212> DNA
<213> Exophiala spinifera

<220>
<221> CDS
<222> (1)...(1389)

<221> misc_feature
<222> (1)...(3)
<223> Extra lysine in K:trAPAO

```

```

<400> 10
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt      48
lys asp asn val ala asp val val val val gly ala gly leu ser gly
1                5                10                15

ctg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc      96
leu glu thr ala arg lys val gln ala ala gly leu ser cys leu val
                20                25                30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgc      144
leu glu ala met asp arg val gly gly lys thr leu ser val gln ser
                35                40                45

ggc ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat      192
gly pro gly arg thr thr ile asn asp leu gly ala ala trp ile asn
                50                55                60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
asp ser asn gln ser glu val ser arg leu phe glu arg phe his leu
65                70                75                80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288

```

10

Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	
85 90 95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag	336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	
100 105 110	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg	384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Gln His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ctg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tgc gac aag aaa gac gcc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tgc att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tgc gca tcc gcc tgt aca gta cga tgc gcc tgc	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tgc gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	

```

305          310          315          320
caa tgc agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac 1008
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga 1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tcc gtc tgg 1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
          355          360          365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag 1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380

ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa 1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
          385          390          395

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt 1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag 1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt 1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca 1389
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

tag 1392

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```

<210> 11
<211> 463
<212> PRT
<213> Exophiala spinifera

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```

<400> 11
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1      5      10      15
Leu Glu Thr Ala Arg Lys Val Gln Ala Gly Leu Ser Cys Leu Val
20     25     30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
35     40     45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
50     55     60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
65     70     75     80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
85     90     95

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Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
      100      105      110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
      115      120      125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
      130      135      140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
      145      150      155      160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
      165      170      175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
      180      185      190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
      195      200      205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
      210      215      220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
      225      230      235      240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
      245      250      255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
      260      265      270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
      275      280      285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
      290      295      300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
      305      310      315      320
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
      325      330      335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
      340      345      350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
      355      360      365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
      370      375      380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
      385      390      395      400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
      405      410      415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
      420      425      430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
      435      440      445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
      450      455      460

```

<210> 12  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Primer sequence designed for cloning DNA into  
 expression vectors, N23256

<400> 12

ggggaattca aagacaaagt tgcggacgtg gtag

34

<210> 13

<211> 34

<212> DNA

<213> Artificial Sequence

<220>

<223> Primer sequence designed for cloning DNA into expression vectors, N23259

<400> 13

ggggcggcgc cctatgctgc tggcaccagg ctag

34

<210> 14

<211> 29

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 3' RACE, N21965

<400> 14

tgggttcgtt accgacaacc ttgtatccc

29

<210> 15

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> Designed oligonucleotide for 5' race, N21968

<400> 15

gagttgggtcc cagacagact ttgttcgt

28

<210> 16

<211> 1673

<212> DNA

<213> Exophiala spinifera

<220>

<221> sig\_peptide

<222> (1)...(267)

<223> yeast alpha mating factor secretion signal.

<221> CDS

<222> (1)...(1662)

<400> 16

atg aga ttt cct tca att ttt act gct gtt tta ttc gca gca tcc tcc

48

Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser

-85

-80

-75

gca tta gct gct cca gtc aac act aca aca gaa gat gaa acg gca caa

96

Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln

-70

-65

-60

```

att cgg gct gaa gct gtc atc ggt tac tca gat tta gaa ggg gat ttc      144
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
      -55                      -50                      -45

gat gtt gct gtt ttg cca ttt tcc aac agc aca aat aac ggg tta ttg      192
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
      -40                      -35                      -30

ttt ata aat act act att gcc agc att gct gct aaa gaa gaa ggg gta      240
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
      -25                      -20                      -15                      -10

tct ctc gag aaa aga gag gct gaa gct gaa ttc aaa gac aac gtt gcg      288
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
                        -5                      1                      5

gac gtg gta gtg ggg ggc gct ggc ttg agc ggt ttg gag acg gca cgc      336
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
      10                      15                      20

aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat      384
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
      25                      30                      35

cgt gta ggg gga aag act ctg agc gta caa tgc ggt ccc ggc agg acg      432
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
      40                      45                      50                      55

act atc aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc      480
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
      60                      65                      70

gaa gta tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag      528
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
      75                      80                      85

agg acg act gga aat tca atc cat caa gca caa gac ggt aca acc act      576
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
      90                      95                      100

aca gct cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca      624
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
      105                      110                      115

ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc      672
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
      120                      125                      130                      135

ctt caa gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg      720
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
      140                      145                      150

agc ttc gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc      768
Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
      155                      160                      165

ggc gta gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac      816

```

15

Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His	
170 175 180	
gag atc agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt	364
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly	
185 190 195	
ctc agt aat att ttc tcc gac aag aaa gac ggc ggg cag tat atg cga	912
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg	
200 205 210 215	
tgc aaa aca ggt atg cag tcc att tgc cat gcc atg tca aag gaa ctt	960
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu	
220 225 230	
gtt cca ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag	1008
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln	
235 240 245	
tcc gca tcc ggc tgt aca gta cga tcc gcc tcc ggc gcc gtg ttc cga	1056
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg	
250 255 260	
agc aaa aag gtg gtg gtt tcc tta ccc aca acc ttc tat ccc acc ttc	1104
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu	
265 270 275	
aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttc ggc gaa aat	1152
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn	
280 285 290 295	
tct atc ctg gcc tac tat agc aag ata gtc ttc gta tgg gac aag ccg	1200
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro	
300 305 310	
tgg tgg cgc gaa caa ggc ttc tcc ggc gtc ctc caa tcc agc tgt gac	1248
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp	
315 320 325	
ccc atc tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg	1296
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp	
330 335 340	
tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa	1344
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln	
345 350 355	
cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca	1392
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala	
360 365 370 375	
gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc	1440
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu	
380 385 390	
gaa atc gag tgg tcc aag cag cag tat ttc caa gga gct ccg agc gcc	1488
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala	
395 400 405	



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gtc tat ggg ctg aac gat ctc atc aca ctg ggt tgc gcg ctc aga acg      1536
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
      410                      415                      420

ccg ttc aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg      1584
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
      425                      430                      435

aaa ggg tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca      1632
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
      440                      445                      450                      455

gaa gtt gtg gct agc ctg gtg cca gca gca tagggggccg c      1673
Glu Val Val Ala Ser Leu Val Pro Ala Ala
      460                      465

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<210> 17
<211> 554
<212> PRT
<213> Exophiala spinifera

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<220>
<221> SIGNAL
<222> (1)...(89)

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<400> 17
Met Arg Phe Pro Ser Ile Phe Thr Ala Val Leu Phe Ala Ala Ser Ser
      -85                      -80                      -75
Ala Leu Ala Ala Pro Val Asn Thr Thr Glu Asp Glu Thr Ala Gln
      -70                      -65                      -60
Ile Pro Ala Glu Ala Val Ile Gly Tyr Ser Asp Leu Glu Gly Asp Phe
      -55                      -50                      -45
Asp Val Ala Val Leu Pro Phe Ser Asn Ser Thr Asn Asn Gly Leu Leu
      -40                      -35                      -30
Phe Ile Asn Thr Thr Ile Ala Ser Ile Ala Ala Lys Glu Glu Gly Val
      -25                      -20                      -15                      -10
Ser Leu Glu Lys Arg Glu Ala Glu Ala Glu Phe Lys Asp Asn Val Ala
      -5                      -1                      5
Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg
      10                      15                      20
Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp
      25                      30                      35
Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr
      40                      45                      50                      55
Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser
      60                      65                      70
Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln
      75                      80                      85
Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr
      90                      95                      100
Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala
      105                      110                      115
Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser
      120                      125                      130                      135
Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val
      140                      145                      150

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```

Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu
      155      160      165
Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His
      170      175      180
Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly
      185      190      195
Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg
200      205      210      215
Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu
      220      225      230
Val Pro Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln
      235      240      245
Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg
      250      255      260
Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu
      265      270      275
Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn
280      285      290      295
Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro
      300      305      310
Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp
      315      320      325
Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp
      330      335      340
Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln
      345      350      355
Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala
360      365      370      375
Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu
      380      385      390
Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala
      395      400      405
Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr
      410      415      420
Pro Phe Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp
      425      430      435
Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala
440      445      450      455
Glu Val Val Ala Ser Leu Val Pro Ala Ala
      460      465

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<210> 18  
 <211> 2079  
 <212> DNA  
 <213> Unknown

<220>  
 <223> GST:K:trAPAO 2079 nt. Translation starting at nt 1  
 - 687, gst fusion + polylinker, 688-2076,  
 K:trAPAO, extra lysine underlined; 2077-2079, stop  
 codon. For bacterial expression.

<221> CDS  
 <222> (1)...(2076)

<221> misc\_feature  
 <222> (1)...(687)

<223> gst fusion + polylinker

<221> misc\_feature

<222> (688)...(2076)

<223> K:trAPAO

<221> misc\_feature

<222> (688)...(690)

<223> Extra lysine

<400> 18

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc	48
Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro	
1 5 10 15	
act cga cct ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg	96
Thr Arg Leu Leu Leu Glu Tyr Leu Glu Lys Tyr Glu Glu His Leu	
20 25 30	
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg	144
Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu	
35 40 45	
ggg ttg gag ttt ccc aac cct cct tat tat att gat ggt gat gtt aaa	192
Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys	
50 55 60	
cta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac	240
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn	
65 70 75 80	
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa	288
Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu	
85 90 95	
gga gcg gtt ttg gat att aga tac ggt gtt tgg aga att gca tat agt	336
Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser	
100 105 110	
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa	384
Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu	
115 120 125	
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat	432
Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn	
130 135 140	
ggg gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat	480
Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp	
145 150 155 160	
gtt gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta	528
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	

ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tgg gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc aaa gac aac gtt gcg gac gtg gta gtg gtg ggc Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly 225 230 235 240	720
gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc ggt Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly 245 250 255	768
ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg gga aag act Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr 260 265 270	816
ctg agc gta caa tgg ggt ccc ggc agg acg act atc aac gac ctc ggc Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly 275 280 285	864
gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc aga ttg ttt Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe 290 295 300	912
gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat tca Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser 305 310 315 320	960
atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt gac Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp 325 330 335	1008
tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg gaa ctc ctc ccc Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro 340 345 350	1056
gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag gcg Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala 355 360 365	1104
agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac tgt Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys 370 375 380	1152
gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag atc Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile 385 390 395 400	1200
aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctt ttt Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe 405 410 415	1248
ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc tgg 20	1296

Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser	
420 425 430	
gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg cag	1344
Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln	
435 440 445	
tgc att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg cac	1392
Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His	
450 455 460	
ctc aac acc ccc gtc gct gaa att gag cag tgc gca tcc ggc tgt aca	1440
Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr	
465 470 475 480	
gta cga tgc gcc tgc ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt	1488
Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val	
485 490 495	
tgc tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct ctt	1536
Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu	
500 505 510	
ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac tat	1584
Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr	
515 520 525	
agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa ggc	1632
Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly	
530 535 540	
ttc tgc ggc gtc ctc caa tgc agc tgt gac ccc atc tca ttc gcc aga	1680
Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg	
545 550 555 560	
gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc atg	1728
Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met	
565 570 575	
gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta cga	1776
Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg	
580 585 590	
caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc ggg	1824
Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly	
595 600 605	
gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgc aag	1872
Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys	
610 615 620	
cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ctg aac gat	1920
Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp	
625 630 635 640	
ctc atc aca ctg ggt tgc gcg ctc aga acg ccg ttc aag agt gtt cat	1968
Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His	
645 650 655	

ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa ggg 2016  
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 660 665 670

gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg gct agc ctg 2064  
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 675 680 685

gtg cca gca gca tag 2079  
 Val Pro Ala Ala  
 690

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 <211> 692  
 <212> PRT  
 <213> Unknown

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 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160  
 Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
 165 170 175  
 Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
 180 185 190  
 Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
 195 200 205  
 Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
 210 215 220  
 Gly Ser Pro Glu Phe Lys Asp Asn Val Ala Asp Val Val Val Val Gly  
 225 230 235 240  
 Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly  
 245 250 255  
 Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr  
 260 265 270  
 Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly  
 275 280 285  
 Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe  
 290 295 300

Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser  
 305 310 315 320  
 Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp  
 325 330 335  
 Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro  
 340 345 350  
 Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala  
 355 360 365  
 Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys  
 370 375 380  
 Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile  
 385 390 395 400  
 Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu Phe  
 405 410 415  
 Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser  
 420 425 430  
 Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln  
 435 440 445  
 Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His  
 450 455 460  
 Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr  
 465 470 475 480  
 Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val Val  
 485 490 495  
 Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu  
 500 505 510  
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr  
 515 520 525  
 Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly  
 530 535 540  
 Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg  
 545 550 555 560  
 Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met  
 565 570 575  
 Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg  
 580 585 590  
 Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly  
 595 600 605  
 Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys  
 610 615 620  
 Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp  
 625 630 635 640  
 Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His  
 645 650 655  
 Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly  
 660 665 670  
 Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu  
 675 680 685  
 Val Pro Ala Ala  
 690

<210> 20  
 <211> 1464  
 <212> DNA  
 <213> Unknown

<220>  
 <223> Nucleotide sequence of K:trAPAO translational

fusion with barley alpha amylase signal sequence, for expression and secretion of the mature trAPAO in maize. Nucleotides 1-72, barley alpha amylase signal sequence, nucleotides 73-75, added lysine residue; nucleotides 76 -1464, trAPAO cDNA.

<221> sig\_peptide  
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<223> Barley alpha amylase signal sequence

<221> misc\_feature  
<222> (73)...(1464)  
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<221> CDS  
<222> (1)...(1461)

<221> misc\_feature  
<222> (73)...(75)  
<223> Added lysine residue

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Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
-20 -15 -10

ctc tcc gcc tcc ctc gcc agc ggc aaa gac aac gtt gcg gac gtg gta 96  
Leu Ser Ala Ser Leu Ala Ser Gly Lys Asp Asn Val Ala Asp Val Val  
-5 1 5

gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag 144  
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln  
10 15 20

gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta ggg 192  
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly  
25 30 35 40

gga aag act ctg agc gta caa tcc ggt ccc gcc agg acg act atc aac 240  
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn  
45 50 55

gac ctc gcc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc 288  
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser  
60 65 70

aga ttg ttc gaa aga ttt cat ttg gag gcc gag ctc cag agg acg act 336  
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
75 80 85

gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct cct 384  
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Ala Pro  
90 95 100

tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctc gcg gaa 432  
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
105 110 115 120



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ctc ctc ccc gta cgg cct cag ctg atc gaa gag cat agc ctt caa gac      480
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
125                               130                               135

ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg      528
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
140                               145                               150

cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca      576
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
155                               160                               165

aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc      624
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
170                               175                               180

atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat      672
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185                               190                               195                               200

att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca      720
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
205                               210                               215

ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc      768
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
220                               225                               230

tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc      816
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
235                               240                               245

ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag      864
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
250                               255                               260

gtg gtg gct tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca      912
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265                               270                               275                               280

cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg      960
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
285                               290                               295

ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc     1008
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
300                               305                               310

gaa caa gcc ttc tcg gcc gtc ctc caa tcg agc tgt gac ccc atc tca     1056
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
315                               320                               325

ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc     1104
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
330                               335                               340

tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag     1152
25

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Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345                      350                      355                      360

cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag      1200
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
                      365                      370                      375

aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtc ctc gaa atc gag      1248
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
                      380                      385                      390

tgg tcg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg      1296
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
                      395                      400                      405

ctg aac gat ctc atc aca ctg ggt tcg gcg ctc aga acg ccg ttc aag      1344
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
                      410                      415                      420

agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg tat      1392
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
425                      430                      435                      440

atg gaa ggg gcc ata cga tcg ggt caa cga ggt gct gca gaa gtt gtg      1440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
                      445                      450                      455

gcc agc ctg gtg cca gca gca tag      1464
Ala Ser Leu Val Pro Ala Ala
                      460

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 <212> PRT  
 <213> Unknown

<220>  
 <221> SIGNAL  
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                      -5                      1                      5
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
10                      15                      20
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
25                      30                      35                      40
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
                      45                      50                      55
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser
60                      65                      70
Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr
75                      80                      85
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro

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      90              95              100
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu
105              110              115              120
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp
      125              130              135
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala
      140              145              150
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala
      155              160              165
Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser
      170              175              180
Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn
185              190              195              200
Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr
      205              210              215
Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly
      220              225              230
Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser
      235              240              245
Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys
250              255              260
Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser
265              270              275              280
Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu
      285              290              295
Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg
      300              305              310
Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser
      315              320              325
Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr
330              335              340
Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys
345              350              355              360
Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu
      365              370              375
Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu
      380              385              390
Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly
395              400              405
Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys
410              415              420
Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr
425              430              435              440
Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val
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Ala Ser Leu Val Pro Ala Ala
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<210> 22
<211> 1803
<212> DNA
<213> Exophiala spinifera

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<220>
<221> CDS
<222> (1)...(1800)

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<400> 22

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gca ggg tat tct cac gtc ggc gta ggc cca gac gga ggg agg tat gtg	96
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
20 25 30	
aca ata gct gga cag att gga caa gac gct tgg ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
50 55 60	
ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
65 70 75 80	
tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
100 105 110	
cca gtg tgg gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
115 120 125	
acg gcg ctg gtg ccg gga cac acg acc cca gac aac gtt gcg gac gtg	432
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
130 135 140	
gta gtg gtg ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gcc	480
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val	
145 150 155 160	
cag gcc gcc ggt ctg tcc tgc ctc gtt ctt gag gcg atg gat cgt gta	528
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
165 170 175	
ggg gga aag act ctg agc gta caa tgg ggt ccc ggc agg acg act atc	576
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
180 185 190	
aac gac ctc ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val	
195 200 205	
tcc aga ttg ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg	672
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	
210 215 220	
act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct	720
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala	
28	

225	230	235	240	
cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg				768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala				
	245	250	255	
gaa ctc ctc ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa				816
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln				
	260	265	270	
gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc				864
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe				
	275	280	285	
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta				912
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val				
	290	295	300	
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc				960
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile				
	305	310	315	320
agc atg ctt ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt				1008
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser				
	325	330	335	
aat att ttc tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa				1056
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys				
	340	345	350	
aca ggt atg cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca				1104
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro				
	355	360	365	
ggc tca gtg cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca				1152
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala				
	370	375	380	
tcc ggc tgt aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa				1200
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys				
	385	390	395	400
aag gtg gtg gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt				1248
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe				
	405	410	415	
tca cca cct ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc				1296
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile				
	420	425	430	
ctg ggc tac tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg				1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp				
	435	440	445	
cgc gaa caa ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc				1392
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile				
	450	455	460	

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tca ttt gcc aga gat acc agc atc gac gtc gat cga caa tgg tcc att 1440
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
465                      470                      475                      480

acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc 1488
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
                      485                      490                      495

aag cag gta cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac 1536
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
                      500                      505                      510

gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc 1584
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
                      515                      520                      525

gag tgg tgg aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat 1632
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
                      530                      535                      540

ggg ctg aac gat ctc atc aca ctg ggt tgg gcg ctc aga acg ccg ttc 1680
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545                      550                      555                      560

aag agt gtt cat ttc gtt gga acg gag acg tct tta gtt tgg aaa ggg 1728
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
                      565                      570                      575

tat atg gaa ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt 1776
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
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Val Ala Ser Leu Val Pro Ala Ala
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<211> 600
<212> PRT
<213> Exophiala spinifera

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20     25     30
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35     40     45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50     55     60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr
65     70     75     80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85     90     95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100    105    110
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
30

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115	120	125
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		
130	135	140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val		
145	150	155
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val		
165	170	175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile		
180	185	190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val		
195	200	205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr		
210	215	220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala		
225	230	235
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala		
245	250	255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln		
260	265	270
Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe		
275	280	285
Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val		
290	295	300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile		
305	310	315
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser		
325	330	335
Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys		
340	345	350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro		
355	360	365
Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala		
370	375	380
Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys		
385	390	395
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe		
405	410	415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile		
420	425	430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp		
435	440	445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile		
450	455	460
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile		
465	470	475
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser		
485	490	495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr		
500	505	510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile		
515	520	525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr		
530	535	540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe		
545	550	555
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly		
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Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val		

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 Val Ala Ser Leu Val Pro Ala Ala  
 595 600

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 <212> DNA  
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 espl mat: an artificial spacer sequence and  
 K:trAPAO

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 -20 -15 -10  
 ctc tcc gcc tcc ctc gcc agc ggc gct cct act gtc aag att gat gct 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Ala Pro Thr Val Lys Ile Asp Ala  
 -5 1 5  
 ggg atg gtg gtc gcc acg act act act gtc ccc gcc acc act ggc acc 144  
 Gly Met Val Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr  
 10 15 20  
 gtc agc gag ttc ttg gcc gtt cct ttt gcc gcc tct ccg aca cga ttt 192  
 Val Ser Glu Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe  
 25 30 35 40  
 ggc cct cct act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act 240  
 Ala Pro Pro Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr  
 45 50 55



gca tat ggt cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctc Ala Tyr Gly Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu 60 65 70	288
cgt gag att acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt Arg Glu Ile Thr Met Ala Trp Phe Asn Thr Pro Pro Ser Ala Gly 75 80 85	336
gaa agt gag gac tgc ctg aac ctc aac atc tac gtc cca gga act gag Glu Ser Glu Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu 90 95 100	384
aac aca aac aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa Asn Thr Asn Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu 105 110 115 120	432
tat ggt tgg aat tca ttc cac ctt tac gac ggg gct agt ttc gca gcc Tyr Gly Trp Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala 125 130 135	480
aat cag gat gtc atc gcc gtg acc atc aac tac aga acg aac att ctg Asn Gln Asp Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu 140 145 150	528
ggg ttc cct gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg Gly Phe Pro Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly 155 160 165	576
ttc cta gac caa agg ttc gct ttg gat tgg gta cag ccg aac atc gca Phe Leu Asp Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala 170 175 180	624
gcc ttc gcc ggt gat cct cga aag gtc aca ata ttt ggg cag agt gcg Ala Phe Gly Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala 185 190 195 200	672
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ccc ttc cga gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc Pro Phe Arg Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe 220 225 230	768
ccc aag gga gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc Pro Lys Gly Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu 235 240 245	816
aac tgt acc acc agt atc gac atc ttg agt tgt atg aga aga gtc gat Asn Cys Thr Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp 250 255 260	864
ctc gcc act ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag Leu Ala Thr Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu 265 270 275 280	912
tac acg ttg gac aac gta acg gct gtg tac cgt tct gaa acg gct cgc	960

Tyr Thr Leu Asp Asn Val Thr Ala Val Tyr Arg Ser Glu Thr Ala Arg	
285 290 295	
acg act ggt gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc	1008
Thr Thr Gly Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala	
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Asn Asp Gly Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr	
315 320 325	
ctc gag gag gca atc cgg aat cag ccc gac ctt tac cag acc ctc ctt	1104
Leu Glu Glu Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu	
330 335 340	
gga gca tat ccc att gga tcc cca ggg atc gga tgg cct caa gat cag	1152
Gly Ala Tyr Pro Ile Gly Ser Pro Gly Ile Ser Pro Gln Asp Gln	
345 350 355 360	
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Ile Ala Ala Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile	
365 370 375	
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Val Ala Gln Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr	
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Tyr Asn Ala Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val	
395 400 405	
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Tyr His Ser Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala	
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Ser Ala Thr Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala	
425 430 435 440	
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Trp Ala Ala Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln	
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Val Pro Asn Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val	
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Asp Val Ser Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg	
475 480 485	
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Tyr Tyr Thr Glu Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly	
490 495 500	
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act gga aat tca atc cat caa gca caa gac ggt aca acc act aca gct Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala 605 610 615	1920
ccr tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala 620 625 630	1968
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gac ctc aag gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe 650 655 660	2064
gcg cac tac tgt gag aag gaa cta aac ttg cct gct gtt ctc gcc gta Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val 665 670 675 680	2112
gca aac cag atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile 685 690 695	2160
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Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala	
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe	
780 785 790	
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795 800 805	
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Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp	
810 815 820	
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Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile	
825 830 835 840	
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Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile	
845 850 855	
acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc	2688
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser	
860 865 870	
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Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr	
875 880 885	
gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc	2784
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890 895 900	
gag tgg tgc aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat	2832
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr	
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Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe	
925 930 935	
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Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly	
940 945 950	
tat atg gaa ggg gcc ata cga tgc ggt caa cga ggt gct gca gaa gtt	2976
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val	
955 960 965	
gtg gct agc ctg gtg cca gca gca tag	3003
Val Ala Ser Leu Val Pro Ala Ala	

970

975

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 <212> PRT  
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&lt;400&gt; 25

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Leu	Ser	Ala	Ser	Leu	Ala	Ser	Gly	Ala	Pro	Thr	Val	Lys	Ile	Asp	Ala
			-5					1				5			
Gly	Met	Val	Val	Gly	Thr	Thr	Thr	Thr	Val	Pro	Gly	Thr	Thr	Ala	Thr
	10				15					20					
Val	Ser	Glu	Phe	Leu	Gly	Val	Pro	Phe	Ala	Ala	Ser	Pro	Thr	Arg	Phe
	25				30				35					40	
Ala	Pro	Pro	Thr	Arg	Pro	Val	Pro	Trp	Ser	Thr	Pro	Leu	Gln	Ala	Thr
			45					50					55		
Ala	Tyr	Gly	Pro	Ala	Cys	Pro	Gln	Gln	Phe	Asn	Tyr	Pro	Glu	Glu	Leu
			60					65					70		
Arg	Glu	Ile	Thr	Met	Ala	Trp	Phe	Asn	Thr	Pro	Pro	Pro	Ser	Ala	Gly
	75					80					85				
Glu	Ser	Glu	Asp	Cys	Leu	Asn	Leu	Asn	Ile	Tyr	Val	Pro	Gly	Thr	Glu
	90				95						100				
Asn	Thr	Asn	Lys	Ala	Val	Met	Val	Trp	Ile	Tyr	Gly	Gly	Ala	Leu	Glu
	105				110					115				120	
Tyr	Gly	Trp	Asn	Ser	Phe	His	Leu	Tyr	Asp	Gly	Ala	Ser	Phe	Ala	Ala
			125						130				135		
Asn	Gln	Asp	Val	Ile	Ala	Val	Thr	Ile	Asn	Tyr	Arg	Thr	Asn	Ile	Leu
			140					145					150		
Gly	Phe	Pro	Ala	Ala	Pro	Gln	Leu	Pro	Ile	Thr	Gln	Arg	Asn	Leu	Gly
	155					160					165				
Phe	Leu	Asp	Gln	Arg	Phe	Ala	Leu	Asp	Trp	Val	Gln	Arg	Asn	Ile	Ala
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Ala	Phe	Gly	Gly	Asp	Pro	Arg	Lys	Val	Thr	Ile	Phe	Gly	Gln	Ser	Ala
	185				190					195				200	
Gly	Gly	Arg	Ser	Val	Asp	Val	Leu	Leu	Thr	Ser	Met	Pro	His	Asn	Pro
			205						210				215		
Pro	Phe	Arg	Ala	Ala	Ile	Met	Glu	Ser	Gly	Val	Ala	Asn	Tyr	Asn	Phe
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Pro	Lys	Gly	Asp	Leu	Ser	Glu	Pro	Trp	Asn	Thr	Thr	Val	Gln	Ala	Leu
	235					240						245			
Asn	Cys	Thr	Thr	Ser	Ile	Asp	Ile	Leu	Ser	Cys	Met	Arg	Arg	Val	Asp
	250				255					260					
Leu	Ala	Thr	Leu	Met	Asn	Thr	Ile	Glu	Gln	Leu	Gly	Leu	Gly	Phe	Glu
	265				270					275				280	
Tyr	Thr	Leu	Asp	Asn	Val	Thr	Ala	Val	Tyr	Arg	Ser	Glu	Thr	Ala	Arg
			285					290					295		
Thr	Thr	Gly	Asp	Ile	Ala	Arg	Val	Pro	Val	Leu	Val	Gly	Thr	Val	Ala
			300					305					310		
Asn	Asp	Gly	Leu	Leu	Phe	Val	Leu	Gly	Glu	Asn	Asp	Thr	Gln	Ala	Tyr
	315						320					325			
Leu	Glu	Glu	Ala	Ile	Pro	Asn	Gln	Pro	Asp	Leu	Tyr	Gln	Thr	Leu	Leu

37

330		335		340
Gly Ala Tyr Pro Ile	Gly Ser Pro Gly Ile	Gly Ser Pro Gln Asp Gln		
345	350	355		360
Ile Ala Ala Ile Glu Thr	Glu Val Arg Phe Gln Cys Pro Ser Ala Ile			
	365	370		375
Val Ala Gln Asp Ser Arg Asn Arg	Gly Ile Pro Ser Trp Arg Tyr Tyr			
	380	385		390
Tyr Asn Ala Thr Phe Glu Asn Leu	Glu Leu Phe Pro Gly Ser Glu Val			
	395	400		405
Tyr His Ser Ser Glu Val Gly Met Val	Phe Gly Thr Tyr Pro Val Ala			
	410	415		420
Ser Ala Thr Ala Leu Glu Ala Gln Thr	Ser Lys Tyr Met Gln Gly Ala			
	425	430		435
Trp Ala Ala Phe Ala Lys Asn Pro Met	Asn Gly Pro Gly Trp Lys Gln			
	445	450		455
Val Pro Asn Val Ala Ala Leu Gly Ser	Pro Gly Lys Ala Ile Gln Val			
	460	465		470
Asp Val Ser Pro Ala Thr Ile Asp	Gln Arg Cys Ala Leu Tyr Thr Arg			
	475	480		485
Tyr Tyr Thr Glu Leu Gly Thr Ile Ala	Pro Arg Thr Phe Gly Gly Gly			
	490	495		500
Ser Gly Gly Gly Ser Gly Gly Gly Ser	Lys Asp Asn Val Ala Asp Val			
	505	510		515
Val Val Val Gly Ala Gly Leu Ser Gly	Leu Glu Thr Ala Arg Lys Val			
	525	530		535
Gln Ala Ala Gly Leu Ser Cys Leu Val	Leu Glu Ala Met Asp Arg Val			
	540	545		550
Gly Gly Lys Thr Leu Ser Val Gln Ser	Gly Pro Gly Arg Thr Thr Ile			
	555	560		565
Asn Asp Leu Gly Ala Ala Trp Ile Asn	Asp Ser Asn Gln Ser Glu Val			
	570	575		580
Ser Arg Leu Phe Glu Arg Phe His Leu	Glu Gly Glu Leu Gln Arg Thr			
	585	590		595
Thr Gly Asn Ser Ile His Gln Ala Gln	Asp Gly Thr Thr Thr Thr Ala			
	605	610		615
Pro Tyr Gly Asp Ser Leu Leu Ser Glu	Glu Val Ala Ser Ala Leu Ala			
	620	625		630
Glu Leu Leu Pro Val Trp Ser Gln Leu	Ile Glu Glu His Ser Leu Gln			
	635	640		645
Asp Leu Lys Ala Ser Pro Gln Ala Lys	Arg Leu Asp Ser Val Ser Phe			
	650	655		660
Ala His Tyr Cys Glu Lys Glu Leu Asn	Leu Pro Ala Val Leu Gly Val			
	665	670		675
Ala Asn Gln Ile Thr Arg Ala Leu Leu	Gly Val Glu Ala His Glu Ile			
	685	690		695
Ser Met Leu Phe Leu Thr Asp Tyr Ile	Lys Ser Ala Thr Gly Leu Ser			
	700	705		710
Asn Ile Phe Ser Asp Lys Lys Asp Gly	Gly Gln Tyr Met Arg Cys Lys			
	715	720		725
Thr Gly Met Gln Ser Ile Cys His Ala	Met Ser Lys Glu Leu Val Pro			
	730	735		740
Gly Ser Val His Leu Asn Thr Pro Val	Ala Glu Ile Glu Gln Ser Ala			
	745	750		755
Ser Gly Cys Thr Val Arg Ser Ala Ser	Gly Ala Val Phe Arg Ser Lys			
	765	770		775
Lys Val Val Val Ser Leu Pro Thr Thr	Leu Tyr Pro Thr Leu Thr Phe			
	780	785		790
Ser Pro Pro Leu Pro Ala Glu Lys Gln	Ala Leu Ala Glu Asn Ser Ile			

```

      795              800              805
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp
  810              815              820
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
  825              830              835              840
Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile
      845              850              855
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      860              865              870
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
      875              880              885
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
      890              895              900
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
  905              910              915              920
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
      925              930              935
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
      940              945              950
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
      955              960              965
Val Ala Ser Leu Val Pro Ala Ala
  970              975

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<210> 26
<211> 2976
<212> DNA
<213> Unknown

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<220>
<223> Barley alpha amylase signal sequence: BEST1
mature: artificial spacer: and K:trAPAO. For
plant expression.

```

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<221> sig_peptide
<222> (1)...(72)
<223> Barley alpha amylase signal sequence

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<221> mat_peptide
<222> (73)...(1545)
<223> BEST1 mature

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<221> misc_feature
<222> (1546)...(1584)
<223> spacer sequence

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<221> misc_feature
<222> (1585)...(2973)
<223> K:trAPAO

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<221> CDS
<222> (1)...(2973)

```

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<221> misc_feature
<222> (1585)...(1587)
<223> Extra lysine

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<400> 26  
 atg gcc aac aag cac ctg agc ctc tcc ctc ttc ctc gtg ctc ctc gcc 48  
 Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly  
 -20 -15 -10

ctc tcc gcc tcc ctc gcc agc gcc acg gat ttt ccg gtc cgc agg acc 96  
 Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr  
 -5 1 5

gat ctg gcc cag gtt cag gga ctg gcc ggg gac gtg atg agc ttt cgc 144  
 Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg  
 10 15 20

gga ata ccc tat gca gcg ccg ccg gtg gcc ggg ctg cgt tgg aag ccg 192  
 Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro  
 25 30 35 40

ccc caa cac gcc cgg ccc tgg gcg gcc gtt cgc ccc gcc acc caa ttt 240  
 Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe  
 45 50 55

ggc tcc gac tgc ttc gcc gcg gcc tat ctt cgc aaa gcc agc ctc gcc 288  
 Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala  
 60 65 70

ccc gcc gtg agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca 336  
 Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser  
 75 80 85

ggc gct aaa ccc gcc cag tac ccc gtc atg gtc tgg gtc tac gcc gcc 384  
 Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly  
 90 95 100

ggc ttc gcc gcc gcc acg gcc gcc atg ccc tac tac gac gcc gag gcg 432  
 Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala  
 105 110 115 120

ctt gcg cga cag gcc gtc gtc gtg gtg acg ttt aac tat cgg acg aac 480  
 Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn  
 125 130 135

atc ctg gcc ttt ttc gcc cat cct ggt ctc tgc cgc gag agc ccc acc 528  
 Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr  
 140 145 150

gga acc tgc gcc aac tac gcc cta ctc gac att ctc gcc gct ctt cgg 576  
 Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg  
 155 160 165

tgg gtg cag agc aac gcc cgc gcc ttc gga ggg gac ccc gcc cga gtg 624  
 Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val  
 170 175 180

acg gtc ttt ggt gaa tgc gcc gga gcg agc gcg atc gga ctt ctg ctc 672  
 Thr Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu  
 185 190 195 200



```

acc tgc ccg ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt      720
Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser
                205                      210                      215

cca ggg ctg acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tgc      768
Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser
                220                      225                      230

ggc gag cgc ctc gac gcc gat ctt tgc cga ctg cgc tgc acc gac cca      816
Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro
                235                      240                      245

gcc acc ctg atg gcg cgc gcc gac gcg gcc cgc ccg gca tgc cgg gac      864
Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp
                250                      255                      260

ctg cgc agg ccg cgt ccg acc gga ccg atc gtc gat gcc cat gtg ctg      912
Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu
                265                      270                      275                      280

ccg cag acc gac agc gcg gcg atc gcg gcc ggg cag ctg gcc ccg gtt      960
Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val
                285                      290                      295

cgg gtc ctg atc gga acc aat gcc gac gaa ggc cgc gcc ttc ctc ggg     1008
Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly
                300                      305                      310

cgc gcg ccg atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg     1056
Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala
                315                      320                      325

cag ttt ggc gac caa gcc gcc gcc gtg gcg gcc tgc tat ccc ctc gac     1104
Gln Phe Gly Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp
                330                      335                      340

ggc cgg gcc acg ccc aag gaa atg gtc gcg cgc atc ttc gcc gac aat     1152
Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn
                345                      350                      355                      360

cag ttc aat cgg ggg gtc tgc gcc ttc tgc gaa gcg ctt gtg cgc cag     1200
Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln
                365                      370                      375

ggc gcg ccc gtg tgg cgt tat cag ttc aac ggt aat acc gag ggt gga     1248
Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly
                380                      385                      390

aga gcg ccg gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg     1296
Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val
                395                      400                      405

ttc aag ctc gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc     1344
Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro
                410                      415                      420

acc ccc gcc gac cgt gcg ctg ggc caa ctg atg tcc tcc gcc cgg gtc     1392
Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val

```

425	430	435	440	
egg ttc gcc aag aat ggc gac ccc gcc ggg gac gcc ctt acc tgg cct				1440
Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro	445	450	455	
gcc tat tct acg ggc aag tgg acc atg aca ttc ggt ccc gag ggc cgc				1488
Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg	460	465	470	
gcg gcg gtg gtg tgg ccc gga cct tcc atc ccc cct tgc gcg gat ggc				1536
Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly	475	480	485	
gcc aag gcg ggg ggc gga ggc agc ggc gga ggc agc ggc gga ggc agc				1584
Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser	490	495	500	
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt				1632
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly	505	510	515	520
tgg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtc				1680
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val	525	530	535	
ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tgg				1728
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser	540	545	550	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat				1776
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn	555	560	565	
gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg				1824
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu	570	575	580	
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				1872
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln	585	590	595	600
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				1920
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu	605	610	615	
gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg tct cag ctg				1968
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	620	625	630	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag				2016
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	635	640	645	
egg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac				2064
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	650	655	660	

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ttg cct gct gtt ctc ggc gta gca aac cag atc ace cgc gct ctg ctc      2112
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
665                      670                      675                      680

ggg ggg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc      2160
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                      685                      690                      695

aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac gcc      2208
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                      700                      705                      710

ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc      2256
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
                      715                      720                      725

atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc      2304
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                      735                      740

gcc gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg      2352
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                      750                      755                      760

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc      2400
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                      765                      770                      775

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      2448
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
780                      785                      790

gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc      2496
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                      800                      805

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc      2544
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                      815                      820

caa tcg agc tgt gac ccc atc tca ttt gcc aga gat acc agc atc gac      2592
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                      830                      835                      840

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga      2640
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
845                      850                      855

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      2688
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                      865                      870

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      2736
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                      880                      885

ccg gcc aac ggg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa      2784
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln

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      890                      895                      900
gga gct cgc agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      2832
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                      910                      915                      920

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      2880
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                      925                      930                      935

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      2928
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                      940                      945                      950

caa cga ggt gct gca gaa gtt gtg gcc agc ctg gtg cca gca gca      2973
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
                      955                      960                      965

tag      2976

<210> 27
<211> 991
<212> PRT
<213> Unknown

<220>
<221> SIGNAL
<222> (1)...(24)

<400> 27
Met Ala Asn Lys His Leu Ser Leu Ser Leu Phe Leu Val Leu Leu Gly
-20 -15 -10
Leu Ser Ala Ser Leu Ala Ser Gly Thr Asp Phe Pro Val Arg Arg Thr
-5 1 5
Asp Leu Gly Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg
10 15 20
Gly Ile Pro Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro
25 30 35 40
Pro Gln His Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe
45 50 55
Gly Ser Asp Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala
60 65 70
Pro Gly Val Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser
75 80 85
Gly Ala Lys Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly
90 95 100
Gly Phe Ala Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala
105 110 115 120
Leu Ala Arg Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn
125 130 135
Ile Leu Gly Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr
140 145 150
Gly Thr Ser Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg
155 160 165
Trp Val Gln Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val
170 175 180
Trp Val Phe Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu
185 190 195 200

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Thr Ser Pro Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser  
 205 210 215  
 Pro Gly Leu Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser  
 220 225 230  
 Gly Glu Arg Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro  
 235 240 245  
 Ala Thr Leu Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp  
 250 255 260  
 Leu Arg Arg Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu  
 265 270 275 280  
 Pro Gln Thr Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val  
 285 290 295  
 Arg Val Leu Ile Gly Thr Asn Ala Asp Glu Gly Arg Ala Phe Leu Gly  
 300 305 310  
 Arg Ala Pro Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala  
 315 320 325  
 Gln Phe Gly Asp Gln Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp  
 330 335 340  
 Gly Arg Ala Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn  
 345 350 355 360  
 Gln Phe Asn Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln  
 365 370 375  
 Gly Ala Pro Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly  
 380 385 390  
 Arg Ala Pro Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val  
 395 400 405  
 Phe Lys Leu Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro  
 410 415 420  
 Thr Pro Ala Asp Arg Ala Leu Gly Gln Leu Met Ser Ser Ala Trp Val  
 425 430 435 440  
 Arg Phe Ala Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro  
 445 450 455  
 Ala Tyr Ser Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg  
 460 465 470  
 Ala Ala Val Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly  
 475 480 485  
 Ala Lys Ala Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Gly Ser  
 490 495 500  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 505 510 515 520  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 525 530 535  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 540 545 550  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 555 560 565  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 570 575 580  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 585 590 595 600  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Gln  
 605 610 615  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 620 625 630  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 635 640 645  
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 650 655 660

```

Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
565                               570 675 680
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
                               685 690 695
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
                               700 705 710
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
                               715 720 725
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
730                               735 740
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
745                               750 755 760
Gly Ala Val Phe Arg Ser Lys Lys Val Val Ser Leu Pro Thr Thr
                               765 770 775
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                               780 785 790
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
795                               800 805
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
810                               815 820
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
825                               830 835 840
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                               845 850 855
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
860                               865 870
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
875                               880 885
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
890                               895 900
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
905                               910 915 920
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                               925 930 935
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
940                               945 950
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
955                               960 965

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<210> 28  
 <211> 3618  
 <212> DNA  
 <213> Unknown

<220>  
 <223> gst:espl:sp:K:trapao, 3618. 1-687, gst +  
 polylinker; 688-2190, espl mat; 2191-2226 spacer;  
 2227-3615, K:trAPAO, 3616-3618, stop codon. For  
 bacterial expression.

<221> CDS  
 <222> (1)...(3615)

<221> misc\_feature  
 <222> (1)...(687)

<223> ~~gst + polylinker~~

<221> mat\_peptide  
 <222> (688)...(2190)  
 <223> espi1 mat

<221> misc\_feature  
 <222> (2191)...(2226)  
 <223> spacer sequence

<221> misc\_feature  
 <222> (2227)...(3615)  
 <223> K:trAPAO

<221> misc\_feature  
 <222> (2227)...(2229)  
 <223> Extra lysine

<400> 28

atg tcc cct ata cta ggt tat tgg aaa att aag ggc ctt gtg caa ccc 48  
 Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro  
 1 5 10 15

act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg 96  
 Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu  
 20 25 30

tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg 144  
 Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45

ggc ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa 192  
 Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60

tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac 240  
 Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80

atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa 288  
 Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95

gga gcg gtt ttg gat att aga tac ggt gtt tgg aga att gca tat agt 336  
 Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110

aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa 384  
 Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125

atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat 432  
 Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140

ggc gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat 480  
 Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160

gtt gtt tta tac atg gac cca atg tgc cgc gat gcg ttc cca aaa tta 528

Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu	
165 170 175	
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac	576
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr	
180 185 190	
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag ggc tgg caa gcc	624
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala	
195 200 205	
acg ttt ggt ggt ggc gac cat cct cca aaa tcg gat ctg gtt ccg cgt	672
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg	
210 215 220	
gga tcc ccg gaa ttc gct cct act gtc aag att gat gct ggg atg gtg	720
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val	
225 230 235 240	
gtc gcc acg act act act gtc ccc gcc acc act gcg acc gtc agc gag	768
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu	
245 250 255	
ttc ttg gcc gtt cct ttt gcc gcc tct ccg aca cga ttt gcg cct cct	816
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro	
260 265 270	
act cgt ccc gtg cct tgg tca acg cct ttg caa gcc act gca tat ggt	864
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly	
275 280 285	
cca gca tgc cct caa caa ttc aat tac ccc gaa gaa ctg cgt gag att	912
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile	
290 295 300	
acg atg gcc tgg ttc aat aca ccg ccc ccg tca gct ggt gaa agt gag	960
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu	
305 310 315 320	
gac tgc ctg aac ctg aac atc tac gtc cca gga act gag aac aca aac	1008
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn	
325 330 335	
aaa gcc gtc atg gtt tgg ata tac ggt gga gcg ctg gaa tat ggt tgg	1056
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp	
340 345 350	
aat tca ttc cac ctg tac gac ggg gct agt ttc gca gcc aat cag gat	1104
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp	
355 360 365	
gtc atc gcc gtg acc atc aac tac aga acg aac att ctg ggg ttc cct	1152
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro	
370 375 380	
gct gcc cct cag ctt cca ata aca cag cga aat ctg ggg ttc cta gac	1200
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp	
385 390 395 400	



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ggg gat cct cga aag gtc aca ata ttt ggg cag agt gcg ggg ggc aga Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg 420 425 430	1296
agt gtc gac gtc ctc ttg acg tct atg cca cac aac cca ccc ttc cga Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg 435 440 445	1344
gca gca atc atg gag tcc ggt gtg gct aac tac aac ttc ccc aag gga Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly 450 455 460	1392
gat ttg tcc gaa cct tgg aac acc act gtt caa gct ctc aac tgt acc Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr 465 470 475 480	1440
acc agt atc gac atc ttg agt tgt atg aga aga gtc gat ctc gcc act Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr 485 490 495	1488
ctg atg aac acg atc gag caa ctc gga ctt ggg ttt gag tac acg ttg Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu 500 505 510	1536
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gac att gct cgt gta cct gtt ctc gtc ggg acg gtg gcc aac gac gga Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly 530 535 540	1632
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gca atc ccg aat cag ccc gac ctt tac cag act ctc ctt gga gca tat Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr 565 570 575	1728
ccc att gga tcc cca ggg atc gga tgg cct caa gat cag att gcc gcc Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala 580 585 590	1776
att gag acc gag gta aga ttc cag tgt cct tct gcc atc gtg gct cag Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln 595 600 605	1824
gac tcc cgg aat cgg ggt atc cct tct tgg cgc tac tac tac aat gcg Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala 610 615 620	1872
acc ttt gag aat ctg gag ctt ttc cct ggg tcc gaa gtg tac cac agc 49	1920

Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser 625 630 635 640	
tct gaa gtc ggg atg gtg ttt ggc acg tat cct gtc gca agt gcg acc Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr 645 650 655	1968
gcc ttg gag gcc cag acg agc aaa tac atg cag ggt gcc tgg gcg gcc Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala 660 665 670	2016
ttt gcc aaa aac ccc atg aat ggg cct ggg tgg aaa caa gtg ccg aat Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn 675 680 685	2064
gtc gcg gcg ctt ggc tca cca ggc aaa gcc atc cag gtt gac gtc tct Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser 690 695 700	2112
cca gcg aca ata gac caa cga tgt gcc ttg tac acg cgt tat tat act Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr 705 710 715 720	2160
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ggc agc ggc gga ggc agc aaa gac aac gtc gcg gac gtg gta gtg gtg Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val 740 745 750	2256
ggc gct ggc ttg agc ggt ttg gag acg gca cgc aaa gtc cag gcc gcc Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala 755 760 765	2304
ggc ctg tcc tgc ctc gtc ctt gag gcg atg gat cgt gta ggg gga aag Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys 770 775 780	2352
act ctg agc gta caa tgc ggt ccc ggc agg acg act atc aac gac ctc Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu 785 790 795 800	2400
ggc gct gcg tgg atc aat gac agc aac caa agc gaa gta tcc agc ttg Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu 805 810 815	2448
ttt gaa aga ttt cat ttg gag ggc gag ctc cag agg acg act gga aat Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn 820 825 830	2496
tca atc cat caa gca caa gac ggt aca acc act aca gct cct tat ggt Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly 835 840 845	2544
gac tcc ttg ctg agc gag gag gtc gca agt gca ctt gcg gaa ctc ctc Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu 850 855 860	2592

ccc gta tgg tct cag ctg atc gaa gag cat agc ctt caa gac ctc aag Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys 865 870 875 880	2640
gcg agc cct cag gcg aag cgg ctc gac agt gtg agc ttc gcg cac tac Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr 885 890 895	2688
tgt gag aag gaa cta aac ttg cct gct gtt ctc ggc gta gca aac cag Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln 900 905 910	2736
atc aca cgc gct ctg ctc ggt gtg gaa gcc cac gag atc agc atg ctc Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu 915 920 925	2784
ttt ctc acc gac tac atc aag agt gcc acc ggt ctc agt aat att ttc Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe 930 935 940	2832
tcg gac aag aaa gac ggc ggg cag tat atg cga tgc aaa aca ggt atg Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met 945 950 955 960	2880
cag tcg att tgc cat gcc atg tca aag gaa ctt gtt cca ggc tca gtg Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val 965 970 975	2928
cac ctc aac acc ccc gtc gct gaa att gag cag tcg gca tcc ggc tgt His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys 980 985 990	2976
aca gta cga tcg gcc tcg ggc gcc gtg ttc cga agc aaa aag gtg gtg Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val 995 1000 1005	3024
gtt tcg tta ccg aca acc ttg tat ccc acc ttg aca ttt tca cca cct Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro 1010 1015 1020	3072
ctt ccc gcc gag aag caa gca ttg gcg gaa aat tct atc ctg ggc tac Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr 1025 1030 1035 1040	3120
tat agc aag ata gtc ttc gta tgg gac aag ccg tgg tgg cgc gaa caa Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln 1045 1050 1055	3168
ggc ttc tcg ggc gtc ctc caa tcg agc tgt gac ccc atc tca ttt gcc Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala 1060 1065 1070	3216
aga gat acc agc atc gac gtc gat cga caa tgg tcc att acc tgt ttc Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe 1075 1080 1085	3264
atg gtc gga gac ccg gga cgg aag tgg tcc caa cag tcc aag cag gta	3312

Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val  
 1090 1095 1100

cga caa aag tct gtc tgg gac caa ctc cgc gca gcc tac gag aac gcc 3360  
 Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala  
 1105 1110 1115 1120

ggg gcc caa gtc cca gag ccg gcc aac gtg ctc gaa atc gag tgg tgg 3408  
 Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser  
 1125 1130 1135

aag cag cag tat ttc caa gga gct ccg agc gcc gtc tat ggg ccg aac 3456  
 Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn  
 1140 1145 1150

gat ctc atc aca ctg ggt tgg ggc ctc aga acg ccg ttc aag agt gtt 3504  
 Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val  
 1155 1160 1165

cat ttc gtc gga acg gag acg tct tta gtt tgg aaa ggg tat atg gaa 3552  
 His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu  
 1170 1175 1180

ggg gcc ata cga tgg ggt caa cga ggt gct gca gaa gtt gtg gct agc 3600  
 Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser  
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ctg gtg cca gca gca tag 3618  
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 <212> PRT  
 <213> Unknown

<400> 29

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 20 25 30

Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu  
 35 40 45

Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
 50 55 60

Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
 65 70 75 80

Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
 85 90 95

Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
 100 105 110

Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
 115 120 125

Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn  
 130 135 140

Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
 145 150 155 160

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Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu
      165      170      175
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr
      180      185      190
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala
      195      200      205
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg
      210      215      220
Gly Ser Pro Glu Phe Ala Pro Thr Val Lys Ile Asp Ala Gly Met Val
225      230      235      240
Val Gly Thr Thr Thr Thr Val Pro Gly Thr Thr Ala Thr Val Ser Glu
      245      250      255
Phe Leu Gly Val Pro Phe Ala Ala Ser Pro Thr Arg Phe Ala Pro Pro
      260      265      270
Thr Arg Pro Val Pro Trp Ser Thr Pro Leu Gln Ala Thr Ala Tyr Gly
      275      280      285
Pro Ala Cys Pro Gln Gln Phe Asn Tyr Pro Glu Glu Leu Arg Glu Ile
      290      295      300
Thr Met Ala Trp Phe Asn Thr Pro Pro Pro Ser Ala Gly Glu Ser Glu
305      310      315      320
Asp Cys Leu Asn Leu Asn Ile Tyr Val Pro Gly Thr Glu Asn Thr Asn
      325      330      335
Lys Ala Val Met Val Trp Ile Tyr Gly Gly Ala Leu Glu Tyr Gly Trp
      340      345      350
Asn Ser Phe His Leu Tyr Asp Gly Ala Ser Phe Ala Ala Asn Gln Asp
      355      360      365
Val Ile Ala Val Thr Ile Asn Tyr Arg Thr Asn Ile Leu Gly Phe Pro
      370      375      380
Ala Ala Pro Gln Leu Pro Ile Thr Gln Arg Asn Leu Gly Phe Leu Asp
385      390      395      400
Gln Arg Phe Ala Leu Asp Trp Val Gln Arg Asn Ile Ala Ala Phe Gly
      405      410      415
Gly Asp Pro Arg Lys Val Thr Ile Phe Gly Gln Ser Ala Gly Gly Arg
      420      425      430
Ser Val Asp Val Leu Leu Thr Ser Met Pro His Asn Pro Pro Phe Arg
      435      440      445
Ala Ala Ile Met Glu Ser Gly Val Ala Asn Tyr Asn Phe Pro Lys Gly
      450      455      460
Asp Leu Ser Glu Pro Trp Asn Thr Thr Val Gln Ala Leu Asn Cys Thr
465      470      475      480
Thr Ser Ile Asp Ile Leu Ser Cys Met Arg Arg Val Asp Leu Ala Thr
      485      490      495
Leu Met Asn Thr Ile Glu Gln Leu Gly Leu Gly Phe Glu Tyr Thr Leu
      500      505      510
Asp Asn Val Thr Ala Val Tyr Arg Ser Gln Thr Ala Arg Thr Thr Gly
      515      520      525
Asp Ile Ala Arg Val Pro Val Leu Val Gly Thr Val Ala Asn Asp Gly
      530      535      540
Leu Leu Phe Val Leu Gly Glu Asn Asp Thr Gln Ala Tyr Leu Glu Glu
545      550      555      560
Ala Ile Pro Asn Gln Pro Asp Leu Tyr Gln Thr Leu Leu Gly Ala Tyr
      565      570      575
Pro Ile Gly Ser Pro Gly Ile Gly Ser Pro Gln Asp Gln Ile Ala Ala
      580      585      590
Ile Glu Thr Glu Val Arg Phe Gln Cys Pro Ser Ala Ile Val Ala Gln
      595      600      605
Asp Ser Arg Asn Arg Gly Ile Pro Ser Trp Arg Tyr Tyr Tyr Asn Ala
610      615      620

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Thr Phe Glu Asn Leu Glu Leu Phe Pro Gly Ser Glu Val Tyr His Ser  
 625 630 635 640  
 Ser Glu Val Gly Met Val Phe Gly Thr Tyr Pro Val Ala Ser Ala Thr  
 645 650 655  
 Ala Leu Glu Ala Gln Thr Ser Lys Tyr Met Gln Gly Ala Trp Ala Ala  
 660 665 670  
 Phe Ala Lys Asn Pro Met Asn Gly Pro Gly Trp Lys Gln Val Pro Asn  
 675 680 685  
 Val Ala Ala Leu Gly Ser Pro Gly Lys Ala Ile Gln Val Asp Val Ser  
 690 695 700  
 Pro Ala Thr Ile Asp Gln Arg Cys Ala Leu Tyr Thr Arg Tyr Tyr Thr  
 705 710 715 720  
 Gln Leu Gly Thr Ile Ala Pro Arg Thr Phe Gly Gly Gly Ser Gly Gly  
 725 730 735  
 Gly Ser Gly Gly Gly Ser Lys Asp Asn Val Ala Asp Val Val Val Val  
 740 745 750  
 Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln Ala Ala  
 755 760 765  
 Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly Gly Lys  
 770 775 780  
 Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu  
 785 790 795 800  
 Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser Arg Leu  
 805 810 815  
 Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn  
 820 825 830  
 Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly  
 835 840 845  
 Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu  
 850 855 860  
 Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp Leu Lys  
 865 870 875 880  
 Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala His Tyr  
 885 890 895  
 Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Ala Asn Gln  
 900 905 910  
 Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Leu  
 915 920 925  
 Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe  
 930 935 940  
 Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met  
 945 950 955 960  
 Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val  
 965 970 975  
 His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys  
 980 985 990  
 Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val Val  
 995 1000 1005  
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro  
 1010 1015 1020  
 Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr  
 1025 1030 1035 1040  
 Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu Gln  
 1045 1050 1055  
 Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala  
 1060 1065 1070  
 Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys Phe  
 1075 1080 1085

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Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln Val
  1090                      1095                      1100
Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala
  1105                      1110                      1115                      1120
Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser
                      1125                      1130                      1135
Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn
                      1140                      1145                      1150
Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser Val
                      1155                      1160                      1165
His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met Glu
                      1170                      1175                      1180
Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala Ser
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Leu Val Pro Ala Ala
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<211> 3591
<212> DNA
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bacterial expression vector pGEX-4T-1 or similar
vector. gst: BEST1:sp:K:trAPAO fusion, 3591 nt.
1-687 gst
+ polylinker, 688-2163, BEST1 mature; 2164-2199,
spacer, 2200-3588, K:trAPAO

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Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln Pro
  1                      5                      10                      15

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55

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act cga ctt ctt ttg gaa tat ctt gaa gaa aaa tat gaa gag cat ttg Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu His Leu 20 25 30	96
tat gag cgc gat gaa ggt gat aaa tgg cga aac aaa aag ttt gaa ttg Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys Phe Glu Leu 35 40 45	144
ggc ttg gag ttt ccc aat ctt cct tat tat att gat ggt gat gtt aaa Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys 50 55 60	192
tta aca cag tct atg gcc atc ata cgt tat ata gct gac aag cac aac Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn 65 70 75 80	240
atg ttg ggt ggt tgt cca aaa gag cgt gca gag att tca atg ctt gaa Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu 85 90 95	288
gga gcg gtt ttg gat att aga tac ggt gtt tgc aga att gca tat agt Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser 100 105 110	336
aaa gac ttt gaa act ctc aaa gtt gat ttt ctt agc aag cta cct gaa Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu 115 120 125	384
atg ctg aaa atg ttc gaa gat cgt tta tgt cat aaa aca tat tta aat Met Leu Lys Met Phe Glu Asp Arg Leu Cys His Lys Thr Tyr Leu Asn 130 135 140	432
ggc gat cat gta acc cat cct gac ttc atg ttg tat gac gct ctt gat Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp 145 150 155 160	480
gtc gtt tta tac atg gac cca atg tgc ctg gat gcg ttc cca aaa tta Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu 165 170 175	528
gtt tgt ttt aaa aaa cgt att gaa gct atc cca caa att gat aag tac Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr 180 185 190	576
ttg aaa tcc agc aag tat ata gca tgg cct ttg cag gcc tgg caa gcc Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala 195 200 205	624
acg ttt ggt ggt ggc gac cat cct cca aaa tgc gat ctg gtt ccg cgt Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg 210 215 220	672
gga tcc ccg gaa ttc acg gat ttt ccg gtc cgc agg acc gat ctg ggc Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly 225 230 235 240	720
cag gtc cag gga ctg gcc ggg gac gtg atg agc ttt cgc gga ata ccc 56	768



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Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro
      245                      250                      255

tat gca gcg ccg ccg gtg ggc ggg ctg cgt tgg aag ccg ccc caa cac      816
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His
      260                      265                      270

gcc cgg ccc tgg gcg ggc gtc cgc ccc gcc acc caa ttt ggc tcc gac      864
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp
      275                      280                      285

tgc ttc ggc gcg gcc tat ctt cgc aaa ggc agc ctc gcc ccc ggc gtg      912
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val
      290                      295                      300

agc gag gac tgt ctt tac ctc aac gta tgg gcg ccg tca ggc gct aaa      960
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys
      305                      310                      315                      320

ccc ggc cag tac ccc gtc atg gtc tgg gtc tac ggc ggc ggc ttc gcc      1008
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala
      325                      330                      335

ggc ggc acg gcc gcc atg ccc tac tac gac ggc gag gcg ctt gcg cga      1056
Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg
      340                      345                      350

cag ggc gtc gtc gtg gtg acg ttt aac tat cgg acg aac atc ctg ggc      1104
Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly
      355                      360                      365

ttt ttc gcc caa cct ggt ctc tcg cgc gag agc ccc acc gga act tcg      1152
Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser
      370                      375                      380

ggc aac tac ggc cta ctc gac att ctc gcc gct ctt cgg tgg gtg cag      1200
Gly Asn Tyr Gly Leu Leu Asp Ile Leu Ala Ala Leu Arg Trp Val Gln
      385                      390                      395                      400

agc aac gcc cgc gcc ttc gga ggg gac ccc ggc cga gtg acg gtc ttt      1248
Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe
      405                      410                      415

ggt gaa tcg gcc gga gcg agc gcg atc gga ctt ctg ctc acc tcg ccg      1296
Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro
      420                      425                      430

ctg agc aag ggt ctc ttc cgt ggc gct atc ctc gaa agt cca ggg ctg      1344
Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu
      435                      440                      445

acg cga ccg ctc gcg acg ctc gcc gac agc gcc gcc tcg ggc gag cgc      1392
Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg
      450                      455                      460

ctc gac gcc gat ctt tcg cga ctg cgc tcg acc gac cca gcc acc ctg      1440
Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu
      465                      470                      475                      480

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ccg cgt ccg acc gga ccg atc gtc gat gcc cat gtg ctg ccg cag acc Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr 500 505 510	1536
gac agc gcg gcg atc gcg gcg ggg cag ctg gcg ccg gtt cgg gtc ctg Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu 515 520 525	1584
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atg gag acg cca gcg gac tac caa gcc tat ctg gag gcg cag ttt gcc Met Glu Thr Pro Ala Asp Tyr Gln Ala Tyr Leu Glu Ala Gln Phe Gly 545 550 555 560	1680
gac caa gcc gcc gcc gtg gcg gcg tgc tat ccc ctc gac gcc cgg gcc Asp Gln Ala Ala Ala Val Ala Ala Cys Tyr Pro Leu Asp Gly Arg Ala 565 570 575	1728
acg ccc aag gaa atg gtc gcg cgc atc ttc gcc gac aat cag ttc aat Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn 580 585 590	1776
cgg ggg gtc tgc gcc ttc tgc gaa gcg ctt gtg cgc cag gcc gcg ccc Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro 595 600 605	1824
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gct acc cac gga gcc gaa att ccc tac gtt ttc ggg gtg ttc aag ctc Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu 625 630 635 640	1920
gac gag ttg ggt ctg ttc gat tgg ccg ccc gag ggg ccc acg ccc gcc Asp Glu Leu Gly Leu Phe Asp Trp Pro Pro Glu Gly Pro Thr Pro Ala 645 650 655	1968
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aag aat gcc gac ccc gcc ggg gac gcc ctt acc tgg cct gcc tat tct Lys Asn Gly Asp Pro Ala Gly Asp Ala Leu Thr Trp Pro Ala Tyr Ser 675 680 685	2064
acg gcc aag tgc acc atg aca ttc ggt ccc gag gcc cgc gcg gcg gtg Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val 690 695 700	2112
gtg tgc ccc gga cct tcc atc ccc cct tgc gcg gat gcc gcc aag gcg 58	2160

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Gly	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Gly	Gly	Gly	Ser	Lys	Asp	Asn		
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Val	Ala	Asp	Val	Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr		
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Arg	Thr	Thr	Ile	Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn		
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caa	agc	gaa	gta	tcc	aga	ttg	ttt	gaa	aga	ttt	cat	ttg	gag	ggc	gag	2448	
Gln	Ser	Glu	Val	Ser	Arg	Leu	Phe	Glu	Arg	Phe	His	Leu	Glu	Gly	Glu		
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ctc	cag	agg	acg	act	gga	aat	tca	atc	cat	caa	gca	caa	gac	ggt	aca	2496	
Leu	Gln	Arg	Thr	Thr	Gly	Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr		
			820					825					830				
acc	act	aca	gct	cct	tat	ggt	gac	tcc	ttg	ctg	agc	gag	gag	ggt	gca	2544	
Thr	Thr	Thr	Ala	Pro	Tyr	Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala		
			835				840					845					
agt	gca	ctt	gcg	gaa	ctc	ctc	ccc	gta	tgg	tct	cag	ctg	atc	gaa	gag	2592	
Ser	Ala	Leu	Ala	Glu	Leu	Leu	Pro	Val	Trp	Ser	Gln	Leu	Ile	Glu	Glu		
	850					855					860						
cat	agc	ctt	caa	gac	ctc	aag	gcg	agc	cct	cag	gcg	aag	cgg	ctc	gac	2640	
His	Ser	Leu	Gln	Asp	Leu	Lys	Ala	Ser	Pro	Gln	Ala	Lys	Arg	Leu	Asp		
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agt	gtg	agc	ttc	gcg	cac	tac	tgt	gag	aag	gaa	cta	aac	ttg	cct	gct	2688	
Ser	Val	Ser	Phe	Ala	His	Tyr	Cys	Glu	Lys	Glu	Leu	Asn	Leu	Pro	Ala		
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gtt	ctc	ggc	gta	gca	aac	cag	atc	aca	cgc	gct	ctg	ctc	ggt	gtg	gaa	2736	
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Ala	His	Glu	Ile	Ser	Met	Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala		
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acc	ggt	ctc	agt	aat	att	ttc	tgc	gac	aag	aaa	gac	ggc	ggg	cag	tat	2832	
Thr	Gly	Leu	Ser	Asn	Ile	Phe	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr		
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ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc ttg tat ccc Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro 995 1000 1005	3024
acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa gca ttg gcg Thr Leu Thr Phe Ser Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala 1010 1015 1020	3072
gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc gta tgg gac Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp 1025 1030 1035 1040	3120
aag ccg tgg tgg cgc gaa caa ggc ttc tgc ggc gtc ctc caa tgc agc Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser 1045 1050 1055	3168
tgt gac ccc atc tca ttc gcc aga gat acc agc atc gac gtc gat cga Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg 1060 1065 1070	3216
caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga cgg aag tgg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp 1075 1080 1085	3264
tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg gac caa ctc Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu 1090 1095 1100	3312
cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag ccg gcc aac Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn 1105 1110 1115 1120	3360
gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa gga gct ccg Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro 1125 1130 1135	3408
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Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly  
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3591

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Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp Gly Asp Val Lys  
50 55 60  
Leu Thr Gln Ser Met Ala Ile Ile Arg Tyr Ile Ala Asp Lys His Asn  
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Met Leu Gly Gly Cys Pro Lys Glu Arg Ala Glu Ile Ser Met Leu Glu  
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Gly Ala Val Leu Asp Ile Arg Tyr Gly Val Ser Arg Ile Ala Tyr Ser  
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Lys Asp Phe Glu Thr Leu Lys Val Asp Phe Leu Ser Lys Leu Pro Glu  
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Gly Asp His Val Thr His Pro Asp Phe Met Leu Tyr Asp Ala Leu Asp  
145 150 155 160  
Val Val Leu Tyr Met Asp Pro Met Cys Leu Asp Ala Phe Pro Lys Leu  
165 170 175  
Val Cys Phe Lys Lys Arg Ile Glu Ala Ile Pro Gln Ile Asp Lys Tyr  
180 185 190  
Leu Lys Ser Ser Lys Tyr Ile Ala Trp Pro Leu Gln Gly Trp Gln Ala  
195 200 205  
Thr Phe Gly Gly Gly Asp His Pro Pro Lys Ser Asp Leu Val Pro Arg  
210 215 220  
Gly Ser Pro Glu Phe Thr Asp Phe Pro Val Arg Arg Thr Asp Leu Gly  
225 230 235 240  
Gln Val Gln Gly Leu Ala Gly Asp Val Met Ser Phe Arg Gly Ile Pro  
245 250 255  
Tyr Ala Ala Pro Pro Val Gly Gly Leu Arg Trp Lys Pro Pro Gln His  
260 265 270  
Ala Arg Pro Trp Ala Gly Val Arg Pro Ala Thr Gln Phe Gly Ser Asp  
275 280 285  
Cys Phe Gly Ala Ala Tyr Leu Arg Lys Gly Ser Leu Ala Pro Gly Val  
290 295 300  
Ser Glu Asp Cys Leu Tyr Leu Asn Val Trp Ala Pro Ser Gly Ala Lys  
305 310 315 320  
Pro Gly Gln Tyr Pro Val Met Val Trp Val Tyr Gly Gly Gly Phe Ala  
325 330 335  
~~Gly Gly Thr Ala Ala Met Pro Tyr Tyr Asp Gly Glu Ala Leu Ala Arg~~  
340 345 350

Gln Gly Val Val Val Val Thr Phe Asn Tyr Arg Thr Asn Ile Leu Gly  
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 Phe Phe Ala His Pro Gly Leu Ser Arg Glu Ser Pro Thr Gly Thr Ser  
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 Ser Asn Ala Arg Ala Phe Gly Gly Asp Pro Gly Arg Val Thr Val Phe  
 405 410 415  
 Gly Glu Ser Ala Gly Ala Ser Ala Ile Gly Leu Leu Leu Thr Ser Pro  
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 Leu Ser Lys Gly Leu Phe Arg Gly Ala Ile Leu Glu Ser Pro Gly Leu  
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 Thr Arg Pro Leu Ala Thr Leu Ala Asp Ser Ala Ala Ser Gly Glu Arg  
 450 455 460  
 Leu Asp Ala Asp Leu Ser Arg Leu Arg Ser Thr Asp Pro Ala Thr Leu  
 465 470 475 480  
 Met Ala Arg Ala Asp Ala Ala Arg Pro Ala Ser Arg Asp Leu Arg Arg  
 485 490 495  
 Pro Arg Pro Thr Gly Pro Ile Val Asp Gly His Val Leu Pro Gln Thr  
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 Asp Ser Ala Ala Ile Ala Ala Gly Gln Leu Ala Pro Val Arg Val Leu  
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 Thr Pro Lys Glu Met Val Ala Arg Ile Phe Gly Asp Asn Gln Phe Asn  
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 Arg Gly Val Ser Ala Phe Ser Glu Ala Leu Val Arg Gln Gly Ala Pro  
 595 600 605  
 Val Trp Arg Tyr Gln Phe Asn Gly Asn Thr Glu Gly Gly Arg Ala Pro  
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 Ala Thr His Gly Ala Glu Ile Pro Tyr Val Phe Gly Val Phe Lys Leu  
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 Thr Gly Lys Ser Thr Met Thr Phe Gly Pro Glu Gly Arg Ala Ala Val  
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 Val Ser Pro Gly Pro Ser Ile Pro Pro Cys Ala Asp Gly Ala Lys Ala  
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 Gly Gly Gly Gly Ser Gly Gly Gly Ser Gly Gly Ser Lys Asp Asn  
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 Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr  
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 Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala  
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 Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly  
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 Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn  
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 Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu  
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Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr  
 820 825 830  
 Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu Val Ala  
 835 840 845  
 Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu  
 850 855 860  
 His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp  
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 Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala  
 885 890 895  
 Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu  
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 Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala  
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 Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr  
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 Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys  
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 Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val  
 980 985 990  
 Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro  
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 Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg  
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 Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro  
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<223> Glyc(-)APAO coding sequence; mutation in putative  
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Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val	
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aca ata gct gga cag att gga caa gac gct tcc ggc gtg aca gac cct	144
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro	
35 40 45	
gcc tac gag aaa cag gtt gcc caa gca ttc gcc aat ctg cga gct tgc	192
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys	
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ctt gct gca gtt gga gcc act tca aac gac gtc acc aag ctc aat tac	240
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr	
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tac atc gtc gac tac gcc ccg agc aaa ctc acc gca att gga gat ggg	288
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly	
85 90 95	
ctg aag gct acc ttt gcc ctt gac agg ctc cct cct tgc acg ctg gtg	336
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val	
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cca gtg tcc gcc ttg tct tca cct gaa tac ctc ttt gag gtt gat gcc	384
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala	
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Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val	
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Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val	
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Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile	
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aac gac ctc gcc gct gcg tgg atc aat gat agc aat cag gcc gaa gta	624
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ala Glu Val	
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Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr	



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cct tat ggt gac tcc ttg ctg agc gag gag gtt gca agt gca ctt gcg			768
Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala			
245	250	255	
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Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln			
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Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe			
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Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val			
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Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile			
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Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser			
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Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys			
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Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro			
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370	375	380	
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Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys			
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Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe			
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Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile			
420	425	430	
ctg gcc tac tat agc aag aca gtc ttc gta tgg gac aag ccg tgg tgg			1344
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp			
435	440	445	

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 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590  
 gtg gct agc ctg gtg cca gca gca tag 1803  
 Val Ala Ser Leu Val Pro Ala Ala \*  
 595 600

<210> 33  
 <211> 600  
 <212> PRT  
 <213> Unknown

<400> 33  
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 1 5 10 15  
 Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
 35 40 45  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60  
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
 65 70 75 80  
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 66

	85		90		95
Leu Lys Ala Thr	Phe Ala Leu Asp Arg	Leu Pro Pro Cys Thr	Leu Val		
100		105		110	
Pro Val Ser Ala	Leu Ser Ser Pro Glu Tyr	Leu Phe Glu Val	Asp Ala		
115		120		125	
Thr Ala Leu Val	Pro Gly His Thr Thr	Pro Asp Asn Val	Ala Asp Val		
130		135		140	
Val Val Val Gly	Ala Gly Leu Ser Gly	Leu Glu Thr	Ala Arg Lys Val		
145		150		155	
Gln Ala Ala Gly	Leu Ser Cys Leu Val	Leu Glu Ala	Met Asp Arg Val		
165		170		175	
Gly Gly Lys Thr	Leu Ser Val Gln Ser Gly	Pro Gly Arg Thr	Thr Thr Ile		
180		185		190	
Asn Asp Leu Gly	Ala Ala Trp Ile Asn Asp	Ser Asn Gln	Ala Glu Val		
195		200		205	
Ser Arg Leu Phe	Glu Arg Phe His Leu Glu Gly	Glu Leu Gln	Arg Thr		
210		215		220	
Thr Gly Asn Ser	Ile His Gln Ala Gln Asp	Gly Thr Thr Thr	Thr Thr Ala		
225		230		235	
Pro Tyr Gly Asp	Ser Leu Leu Ser Glu Glu	Val Ala Ser	Ala Leu Ala		
245		250		255	
Glu Leu Leu Pro	Val Trp Ser Gln Leu Ile	Glu Glu His	Ser Leu Gln		
260		265		270	
Asp Leu Lys Ala	Ser Pro Gln Ala Lys Arg	Leu Asp Ser	Val Ser Phe		
275		280		285	
Ala His Tyr Cys	Glu Lys Glu Leu Asn Leu	Pro Ala Val	Leu Gly Val		
290		295		300	
Ala Asn Gln Ile	Thr Arg Ala Leu Leu Gly	Val Glu Ala	His Glu Ile		
305		310		315	
Ser Met Leu Phe	Leu Thr Asp Tyr Ile Lys	Ser Ala Thr	Gly Leu Ser		
325		330		335	
Asn Ile Phe Ser	Asp Lys Lys Asp Gly Gly	Gln Tyr Met	Arg Cys Lys		
340		345		350	
Thr Gly Met Gln	Ser Ile Cys His Ala Met	Ser Lys Glu	Leu Val Pro		
355		360		365	
Gly Ser Val His	Leu Asn Thr Pro Val	Ala Glu Ile	Glu Gln Ser	Ala	
370		375		380	
Ser Gly Cys Thr	Val Arg Ser Ala Ser Gly	Ala Val Phe	Arg Ser Lys		
385		390		395	
Lys Val Val Val	Ser Leu Pro Thr Thr	Leu Tyr Pro	Thr Leu Thr	Phe	
405		410		415	
Ser Pro Pro Leu	Pro Ala Glu Lys Gln	Ala Leu Ala	Glu Asn Ser	Ile	
420		425		430	
Leu Gly Tyr Tyr	Ser Lys Ile Val Phe	Val Trp Asp	Lys Pro Trp	Trp	
435		440		445	
Arg Glu Gln Gly	Phe Ser Gly Val	Leu Gln Ser	Ser Cys Asp	Pro Ile	
450		455		460	
Ser Phe Ala Arg	Asp Thr Ser Ile Asp	Val Asp Arg	Gln Trp Ser	Ile	
465		470		475	
Thr Cys Phe Met	Val Gly Asp Pro Gly	Arg Lys Trp	Ser Gln Gln	Ser	
485		490		495	
Lys Gln Val Arg	Gln Lys Ser Val Trp	Asp Gln Leu	Arg Ala Tyr		
500		505		510	
Glu Asn Ala Gly	Ala Gln Val Pro Glu	Pro Ala Asn	Val Leu Glu	Ile	
515		520		525	
Glu Trp Ser Lys	Gln Gln Tyr Phe Gln	Gly Ala Pro	Ser Ala Val	Tyr	
530		535		540	
Gly Leu Asn Asp	Leu Ile Thr Leu Gly	Ser Ala Leu	Arg Thr Pro	Phe	

545                      550                      555                      560  
 Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
                                  565                      570                      575  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Glu Arg Gly Ala Ala Glu Val  
                                  580                      585                      590  
 Val Ala Ser Leu Val Pro Ala Ala  
                                  595                      600

<210> 34  
 <211> 37  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> 37-mer oligonucleotide

<400> 34  
 ggggaattca tggcacttgc accgagctac atcaatc

37

<210> 35  
 <211> 1929  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> intron  
 <222> (739)...(811)  
 <221> intron  
 <222> (1134)...(1186)

<400> 35  
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 cacatcgggc taggccc aaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgctttcg gcgtgacaga cccagcctac gagaaacagg ttgccc aagc attcgccaat 180  
 ctgcgagctt gccttgctgc agttggagcc tcctcaaacy acgtcaccaa gctcaattac 240  
 tacatcgctg actacgcccc gagcaaaact accgcaattg gagatgggct gaagtctacc 300  
 tttgcccctg acaggctccc tcccttgacg ctggtgcccag taccggcctt ggcttcacct 360  
 gaatacctct ttgaggttga tgccacggcg ctggtgcccag gacactcgac cccagacaa 420  
 gttagcgagc tggtagtggt gggcgctggc ttgagcggtt tggagacggc accgaaagtc 480  
 caggccgcgc gctgttctcg cctcgctctt gaggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtac aatcggttcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcattt ggaggcgag 660  
 ctccagagga cgaccggaaa ttcaatccat caagcacaaag accgtacac cactacagct 720  
 cottatggtg actcccggt aagcacaaat ccactttgtg atgagacctc tctcgaggtg 780  
 agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgc aa gtgcaattgc 840  
 ggaactcttc cccgtatggt ctacagctgat cgaaggttat agccttgaag accccaaggc 900  
 gaggcctcag gcgagggggc tcgacagtggt gagcttcgcg cactactgtg agcaggacct 960  
 aaacttgcct gctgttctca gcgtggcaaa ccagatcaca cgcgctctgc tgggtgtgga 1020  
 agcccacgag atcagcatgc tttttctcac cgactacatc aagagtgc aa cgggtctcag 1080  
 taatattgtc tcggacaaga aagacggcgg gcagtatatg cgatgc aaaa cagggtgcgtg 1140  
 cgggtgtctc tcaggtaggg gactcgtttc ttagtgggtc tccagggtat gcagtcgatt 1200  
 tgccatgcca tgc aaaaagga acctgttcca ggtcagtgct acctcaaac ccccgctcgt 1260  
 ggaattgagc agtcggcgct cgcctgtata gtacgactcg cctcggggcg cgtgttcoga 1320  
 agcaaaaagg tggtgggttc gttaccgaca acattgtatc ccacettgac attttacca 1380  
 cctcttcccg ccgagaagca agcattggcg gaaaaatcta tccctggcta ctatagcaag 1440  
 atagtctctg tatgggacaa ccdgtgggtg cgcgaaczag gctctctggg cgtctctcaa 1500  
 cagagctgtg accccatctc atttgccaga gataccagca tcgaagtcca tgggcaatgg 1560

```

tccattacct gtttcattggt cggagaccgg ggacggaagt ggtcccaaca gtccaagcag 1620
gtaccgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaangc cggggcccaa 1680
gtcccagagc cggccaactg gctcgaaatc gactggctga acgagcagta ttccaagga 1740
gtcccgagcg ccgtctatgg gctgaacgat ctcatcacac tgggttcggc gctcagaacg 1800
ccgttcaagt gtgttcattt cgttggaacg gagacgtctt tagtttggaa agggatatatg 1860
gaagggggcca tacgatcggg tcaacgaggt gctgcagaag ttgtggctag cctgggtgcca 1920
gcagcatag 1929

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<210> 36  
 <211> 600  
 <212> PRT  
 <213> *Exophiala spinifera*

<400> 36

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Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20     25     30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35     40     45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50     55     60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65     70     75     80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85     90     95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100    105    110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115    120    125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130    135    140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145    150    155    160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165    170    175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180    185    190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195    200    205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210    215    220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225    230    235    240
Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
245    250    255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
260    265    270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
275    280    285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
290    295    300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305    310    315    320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
325    330    335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
340    345    350

```

Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365  
 Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala  
 370 375 380  
 Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
 385 390 395 400  
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
 405 410 415  
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile  
 420 425 430  
 Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp  
 435 440 445  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460  
 Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480  
 Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser  
 485 490 495  
 Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr  
 500 505 510  
 Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile  
 515 520 525  
 Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr  
 530 535 540  
 Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe  
 545 550 555 560  
 Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly  
 565 570 575  
 Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val  
 580 585 590  
 Val Ala Ser Leu Val Pro Ala Ala  
 595 600

<210> 37  
 <211> 1929  
 <212> DNA  
 <213> *Exophiala spinifera*

<220>  
 <221> intron  
 <222> (739)...(811)  
 <221> intron  
 <222> (1134)...(1186)

<400> 37  
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 cacatcggcg taggccccaaa cgaagcgagg tatgtgacaa tagctggaca gattggacaa 120  
 gacgcttttg gcgtgacaga cccagcctac gagaaacagg ttgcccaagc attcgccaat 180  
 ctgcgagcgt gccttgcctgc agtgggagcc tcttcaaaag acgtcagcaa gctcaattac 240  
 tacatcgctc actacgcccc gagcaaaact accgcaattg gagatgggct gaagtctacc 300  
 tttgcccttg acaggctccc tctttgcaag ctggtgcccag taccggcctt ggcctcacct 360  
 gaatacctct ttgaggttga cgcacgggcg ctggtgcccag gacactcgac cccagacaaac 420  
 gttgcggagc tggtagtggt gggcgctggc ttgagcggct tggagacggc accgaaagtc 480  
 caggcgccgc gctctgctcg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540  
 ctgagcgtac aatcggttcc cggcaggacg actatcaacg acctcggcgc tgcgtggatc 600  
 aatgacagca accaaagcga agtatccaga ttgcttgaaa gatttcattt ggaggggcag 660  
 ctccagagga cgaccggaaa tccaatccat caagcacaag acggtacaac cactacagct 720

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ccttatgggtg actccccggt aagcacaatc ccactttgtg atgagacctc tgtcgagtgt 780
agaatacagt cactgactcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
ggaactccctc cccgtatggt ctcagctgat cgaagagtat agccttgaag accccaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgag cactactgtg agaaggacct 960
aaacttgcct gctgttctca gctgtggcaaa ccagatcaca cgcgctctgc tcggtgtgga 1020
agcccaagag atcagcatgc tttttctcac cgactacatc aagagtgcga ccggtctcag 1080
taatatgttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
cggtgtctctc tcaggtaggg gactcgttcc ttagtggtca ttccaggtat gcagtcgatt 1200
tgccatgcca tgtcaaagga acttgttcca ggctcagtgc acctcaacac ccccgctcgt 1260
ggaattgagc agtcggcgtc cggctgtata gtacgatcgg cctcgggggc cgtgttccga 1320
agcaaaaagg tgggtgttcc gttaccgaca acattgtatc ccactttgac attttcacca 1380
cctcttcccg ccgagaagca agcattggcg gaaaaatcta tctcggcta ctatagcaag 1440
atagtcttcg tatgggacaa cccgtgggtg cgcgaacaag gcttctcggt cgtctctcaa 1500
tcgagctgtg accccatctc atttgccaga gataccagca tcgaagtcca tcggcaatgg 1560
tccattacct gtttcatggt cggagaccgg ggacgggaag ggtcccaaca gtccaagcag 1620
gtacgacaaa agtctgtctg ggaccaactc cgcgcagcct acgagaacgc cgggggccaa 1680
gtccagagac cgcccaacgt gctcgaaatc gactgggtcg agcagcagta tttccaagga 1740
gctccgagcg cgtctatggt gctgaacgat ctcacacac tgggttcggc gctcagaacg 1800
ccgttcaagt gtgttcattt cgttggaaac gagacgtctt tagtttgga aggttatatg 1860
gaaggggcca tacgatcggg tcaaccgaggt gctgcagaag ttgtggctag cctcgtgcga 1920
gcagcatag

```

<210> 38  
 <211> 600  
 <212> PRT  
 <213> *Exophiala spinifera*

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<400> 38
Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
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Ala Gly Tyr Ser His Ile Gly Val Gly Pro Asn Glu Ala Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Leu Gly Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Ser Ser Asn Asp Val Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ser Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile
180 185 190
Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val
195 200 205
Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr
210 215 220
Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala
225 230 235 240

```

```

Pro Tyr Gly Asp Ser Pro Leu Ser Glu Glu Val Ala Ser Ala Leu Ala
      245      250      255
Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu Tyr Ser Leu Glu
      260      265      270
Asp Pro Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe
      275      280      285
Ala His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Ser Val
      290      295      300
Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile
305      310      315      320
Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser
      325      330      335
Asn Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys
      340      345      350
Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro
      355      360      365
Gly Ser Val His Leu Asn Thr Pro Val Ala Gly Ile Glu Gln Ser Ala
370      375      380
Ser Gly Cys Ile Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys
385      390      395      400
Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe
      405      410      415
Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile
      420      425      430
Leu Gly Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Asn Pro Trp Trp
      435      440      445
Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile
450      455      460
Ser Phe Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile
465      470      475      480
Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      485      490      495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
500      505      510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
515      520      525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
530      535      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545      550      555      560
Lys Cys Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
      565      570      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
580      585      590
Val Ala Ser Leu Val Pro Ala Ala
595      600

```

```

<210> 39
<211> 1930
<212> DNA
<213> Exophiala spinifera

```

```

<220>
<221> intron
<222> (739)...(811)

```

```

<221> intron
<222> (1134)...(1187)

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<221> misc\_feature  
 <222> (648)...(648)  
 <223> n = A,T,C or G

<400> 39

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gacgcttcgg gcgtgacaga ccttgccctac gagaaacagg ttgcccagc attcgccaat 180
ctgcgagctt gccttgctgc agttggagcc acttcaaacc acgtcaccaa gctcaattac 240
taccatgctg actacgcccc gagcaaacct accgcaattg gagatgggct gaaggctacc 300
tttgcctctg acaggctccc tctttgcacg ctgggtgcag tgtcggcctt gcttcacct 360
gaataacctt ttgaggttga tgcacggcg ctgggtgcgg gacacacgac ccagacaaac 420
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caggccggcg gtctgtcctg cctcgttctt gaggcgatgg atcgtgtagg gggaaagact 540
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aatgacagca accaaagcga agtatccaga ttgtttgaaa gatttcatnt gtagggcgag 660
ctccagagga cgactggaaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggt actccttggg aagcacaatc ccactttgtg atgagacctc tgtcagtggt 780
agaatacagt cactgattcc acttcgtcca gctgagcgag gaggttgcaa gtgcacttgc 840
ggaaactctc ccgttatggg ctccagctgat cgaagagcat agccttcaag acctcaaggc 900
gagccctcag gcgaagcggc tcgacagtgt gagcttcgcg cactactgtg agaaggaact 960
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taaatatttc tcggacaaga aagacggcgg gcagtatatg cgatgcaaaa caggtgcgtg 1140
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aagcaaaaag gtggtgggtt cgttaccgac aaccttgtat cccaccttga cattttcacc 1380
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gatagtcttc gtatgggaca agccttgggt gcgcgaacaa ggcttctcgg gcgtcctcca 1500
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gtccattacc tgtttcatgg tcggagaccc gggacggaaag tggccccaac agtcccagca 1620
ggtacgacaa aagtctgtct gggaccaact ccgcgcagcc tacgagaacg ccggggccca 1680
agtcaccagag ccggccaaag tgctcgaaat cgagtggctg aagcagcagt atttccaaag 1740
agctccgagc gccgtctatg ggtgaaacga tctcatcaca ctgggttcgg cgtcagaac 1800
gccgttcaag agtgttcatt tgcgttgaaac ggagacgtct ttagtttgga aaggglatat 1860
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agcagcatag
  
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<210> 40  
 <211> 598  
 <212> PRT  
 <213> *Exophiala spinifera*

<220>  
 <221> VARIANT  
 <222> (216)...(216)  
 <223> Xaa = Any Amino Acid

<400> 40

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro
 1           5           10           15
Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val
      20           25           30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro
35           40           45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
  
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50	55	60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr		
65	70	75
Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly		80
	85	90
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val		95
	100	105
Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala		110
	115	120
Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val		125
	130	135
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln		140
145	150	155
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly		160
	165	170
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn		175
	180	185
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Ser		190
	195	200
Arg Leu Phe Glu Arg Phe His Xaa Glu Gly Glu Leu Gln Arg Thr Thr		205
	210	215
Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro		220
225	230	235
Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu		240
	245	250
Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln Asp		255
	260	265
Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe Ala		270
	275	280
His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val Asn		285
	290	295
Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met		300
305	310	315
Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile		320
	325	330
Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly		335
	340	345
Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser		350
	355	360
Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly		365
	370	375
Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys Lys Val		380
385	390	395
Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe Ser Pro		400
	405	410
Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile Leu Gly		415
	420	425
Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu		430
	435	440
Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe		445
	450	455
Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile Thr Cys		460
465	470	475
Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln		480
	485	490
Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr Glu Asn		495
	500	505
Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp		510

515                      520                      525  
 Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr Gly Leu  
 530                      535                      540  
 Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Ser  
 545                      550                      555                      560  
 Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
 565                      570                      575  
 Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
 580                      585                      590  
 Ser Leu Val Pro Ala Ala  
 595

<210> 41  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocladiaella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)  
 <221> intron  
 <222> (1134)...(1185)

<400> 41

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cacgtcgggc	taggcccaca	cggagggagg	tatggacaaa	tagctggaca	gattggacaa	120
gacgtctcgg	ccgtgacaga	ccctgcctac	gagaaacagg	ttgccaagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agttggagcc	acttcaaacg	acattacca	gotcaattac	240
tacatcgctg	actacaaccc	gagcaaacct	accgcaattg	gagatgggct	gaaggctacc	300
tttgcctctg	acaggctccc	tccttgccag	ctggtgccag	tgccggccct	ggcttcacct	360
gaataccccc	ttgaggttga	tgccacggcg	ctggttccag	gacactcaac	cccagacaat	420
gttgcggacg	tggtcgtggt	gggcgctggc	ctgagcggtt	tgagagcggc	acgcaaagtc	480
caggctgcgc	ggctgtcctg	cctcggttct	gagggcatgg	atcgtgtggg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggagc	gctatcaatg	acctcgggcg	tgctgtggatc	600
aatgacagca	accaaagcga	agtattccaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaa	acggtacaac	cactacagct	720
ccttatgggtg	attccctggt	aagcacaatt	ccatcttggt	atgagacctc	tgctgtgtgt	780
agaatacagt	cgctgactcc	acatcgctcc	gctgagcgag	gaggttgcaa	gtgcaactcg	840
ggaactccct	cccgcctggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tcgacagtgt	gagcttcgca	cactactgtg	agaaggatct	960
aagcttgcc	gtgttctcgc	gctgtggcaa	ccagatcaca	cgcgctcgc	tcggtgtgga	1020
agcccacgag	atcagcatgc	ttttctctac	cgactacatc	aagagtgcga	ccggtctcag	1080
taatatgtgc	tcggataaga	aagacggtgg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140
tggtgttctc	tcagtgggag	actcgtttct	tagtgggtcat	tcagggtatg	cagtcgcttt	1200
gccatgccat	gtcaaaggaa	cttgttccag	gctcagtgca	cctcaacacc	cccgtcgcgc	1260
aaattgagga	gtcggcatcc	ggctgtacag	tacgatcggc	ctcgggcggc	gtgttccgaa	1320
gtaaaaaggt	ggtggtttcg	tcaccgacaa	ccttgtatcc	cacttgata	ttttcaccac	1380
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cgagctgtga	ccccatctca	tttgccagag	ataccagcat	cgaagtcgat	cggcaatggt	1560
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tacgacagaa	gtctgtctgg	aaccaactcc	cgcgagccta	cgagaacgce	ggggccccag	1680
tcccagagcc	ggccaacgtg	ctcgagatcg	agtggctcgaa	gcagcagtat	ttccaaggag	1740
cgccgagcgt	cgtctatggg	ctgaactgtc	tcaacacact	gggttcggcg	ctcagaacgc	1800
cgttcaaggg	tgttcatttc	gttgggaacgg	agacgtcttt	gtttcgaaa	gggtatatgg	1860
agggggccat	acgatcgggt	cagcgaggcg	ctgcagaagt	tggtggtatg	ctggtgccag	1920
cagcatag						1928

<210> 42  
 <211> 598  
 <212> FRT  
 <213> Rhinoclaadiella atrovirens

<400> 42

Met	Ala	Leu	Ala	Pro	Ser	Tyr	Ile	Asn	Pro	Pro	Asn	Leu	Ala	Ser	Pro
1				5					10					15	
Ala	Gly	Tyr	Ser	His	Val	Gly	Val	Gly	Pro	Asn	Gly	Gly	Arg	Tyr	Ala
			20					25					30		
Thr	Ile	Ala	Gly	Gln	Ile	Gly	Gln	Asp	Ala	Ser	Ala	Val	Thr	Asp	Pro
		35				40						45			
Ala	Tyr	Glu	Lys	Gln	Val	Ala	Gln	Ala	Phe	Ala	Asn	Leu	Arg	Ala	Cys
	50				55						60				
Leu	Ala	Ala	Val	Gly	Ala	Thr	Ser	Asn	Asp	Ile	Thr	Lys	Leu	Asn	Tyr
65					70					75				80	
Tyr	Ile	Val	Asp	Tyr	Asn	Pro	Ser	Lys	Leu	Thr	Ala	Ile	Gly	Asp	Gly
				85					90					95	
Leu	Lys	Ala	Thr	Phe	Ala	Leu	Asp	Arg	Leu	Pro	Pro	Cys	Thr	Leu	Val
		100						105					110		
Pro	Val	Pro	Ala	Leu	Ala	Ser	Pro	Glu	Tyr	Pro	Phe	Glu	Val	Asp	Ala
		115					120						125		
Thr	Ala	Leu	Val	Pro	Gly	His	Ser	Thr	Pro	Asp	Asn	Val	Ala	Asp	Val
	130					135						140			
Val	Val	Val	Gly	Ala	Gly	Leu	Ser	Gly	Leu	Glu	Thr	Ala	Arg	Lys	Val
145					150					155				160	
Gln	Ala	Ala	Gly	Leu	Ser	Cys	Leu	Val	Leu	Glu	Ala	Met	Asp	Arg	Val
			165						170					175	
Gly	Gly	Lys	Thr	Leu	Ser	Val	Gln	Ser	Gly	Pro	Gly	Arg	Thr	Ala	Ile
		180						185					190		
Asn	Asp	Leu	Gly	Ala	Ala	Trp	Ile	Asn	Asp	Ser	Asn	Gln	Ser	Glu	Val
	195						200						205		
Phe	Lys	Leu	Phe	Glu	Arg	Leu	Glu	Gly	Glu	Leu	Gln	Arg	Thr	Thr	Gly
	210					215						220			
Asn	Ser	Ile	His	Gln	Ala	Gln	Asp	Gly	Thr	Thr	Thr	Thr	Ala	Pro	Tyr
225					230					235				240	
Gly	Asp	Ser	Leu	Leu	Ser	Glu	Glu	Val	Ala	Ser	Ala	Leu	Ala	Glu	Leu
			245						250					255	
Leu	Pro	Ala	Trp	Ser	Gln	Leu	Ile	Glu	Glu	His	Ser	Leu	Glu	Asp	Pro
		260						265					270		
Lys	Ala	Ser	Pro	Gln	Ala	Lys	Gln	Leu	Asp	Ser	Val	Ser	Phe	Ala	His
	275						280						285		
Tyr	Cys	Glu	Lys	Asp	Leu	Ser	Leu	Pro	Ala	Val	Leu	Gly	Val	Ala	Asn
	290					295					300				
Gln	Ile	Thr	Arg	Ala	Leu	Gly	Val	Glu	Ala	His	Glu	Ile	Ser	Met	
305					310					315				320	
Leu	Phe	Leu	Thr	Asp	Tyr	Ile	Lys	Ser	Ala	Thr	Gly	Leu	Ser	Asn	Ile
			325						330					335	
Val	Ser	Asp	Lys	Lys	Asp	Gly	Gly	Gln	Tyr	Met	Arg	Cys	Lys	Thr	Gly
		340						345					350		
Met	Gln	Ser	Leu	Cys	His	Ala	Met	Ser	Lys	Glu	Leu	Val	Pro	Gly	Ser
	355						360						365		
Val	His	Leu	Asn	Thr	Pro	Val	Ala	Glu	Ile	Glu	Gln	Ser	Ala	Ser	Gly
	370					375					380				
Cys	Thr	Val	Arg	Ser	Ala	Ser	Gly	Gly	Val	Phe	Arg	Ser	Lys	Cys	Val
385					390					395				400	
Val	Val	Ser	Leu	Pro	Thr	Thr	Leu	Tyr	Pro	Thr	Leu	Ile	Phe	Ser	Pro

405 410 415  
 Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Leu Gly  
 420 425 430  
 Tyr Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp Arg Glu  
 435 440 445  
 Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe  
 450 455 460  
 Ala Arg Asp Thr Ser Ile Glu Val Asp Arg Gln Trp Ser Ile Thr Cys  
 465 470 475 480  
 Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser Lys Gln  
 485 490 495  
 Val Arg Gln Lys Ser Val Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn  
 500 505 510  
 Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile Glu Trp  
 515 520 525  
 Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Val Val Tyr Gly Leu  
 530 535 540  
 Asn Cys Leu Asn Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe Lys Gly  
 545 550 555 560  
 Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly Tyr Met  
 565 570 575  
 Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val Val Ala  
 580 585 590  
 Ser Leu Val Pro Ala Ala  
 595

<210> 43  
 <211> 1928  
 <212> DNA  
 <213> *Rhinocladiaella atrovirens*

<220>  
 <221> intron  
 <222> (739)...(811)  
 <221> intron  
 <222> (1134)...(1186)

<400> 43

atggcaacttg	caccgagcta	catcaatccc	ccaaacctcg	cctccccagc	agggtattcc	60
tacgtcggcg	taggccc aaa	cggaggagg	tatgtgacaa	tagctggaca	gattggacaa	120
gacgcttcgg	cctgacaga	ccttgctac	gagaaacagg	ttgcccagc	attcgccaac	180
ctgcgagctt	gtcttgctgc	agtgaggcc	acttcaaacg	acattacca	gtcaattac	240
tacatcgtcg	actacaaccc	gagcaactc	acgcgaattg	gagatgggct	gaaggctacc	300
tttgcccttg	acaggtcccc	tccttgcaag	ctgggtgccag	tgccggccct	ggcttcaact	360
gaataccctt	ttgaggttga	tgccacggcg	ctgggttccag	gacactcaac	cccagacaat	420
gttccgagac	tggctcgtgt	ggcgctggc	ctggaggggt	tggagacggc	acgcaagtc	480
caggctgcgc	ggctgtcctg	cctcgttctt	gaggcgatgg	atcgtgctgg	gggaaagact	540
ctgagcgtac	aatcgggtcc	cggcaggacg	actatcaatg	acctcggcgc	tgctgggac	600
aatgacagca	accaaagcga	agtattcaaa	ttatttgaaa	gatttcattt	ggagggcgag	660
ctccagagga	cgaccggaaa	ttcaatccat	caagcacaag	acggtacaac	cactacagct	720
ccttatgggt	attccctggt	aagcacaatt	ccatctctgt	atgagacctc	tgctgtgtgt	780
agaatacagt	cgtgactcc	acatcgtcca	gctgagcgag	gaggttgcaa	gtgcactcgc	840
ggaactcctt	ccgcctggt	ctcagctgat	cgaagagcat	agtcttgaag	accccaaggc	900
gagccctcaa	gcgaagcagc	tgcacagtgc	cactactgtg	agaaggact		960
aaacttgctt	gctgttctcg	gcgtggcaaa	ccagatcaca	cgcgctctgc	tcggtgtgga	1020
agcccacgag	atcagcatgt	ctttctctac	cgactacatc	aagagtgcct	ccggtctcag	1080
taatatgttc	tcggataaga	aagacgggtg	gcagtatatg	cgatgcaaaa	caggtgcgtg	1140

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tgggtgtctc tcagtgggag actcggttct tagtgggtcat tccaggtatg cagtcgtttt 1200
gccatgccat gtcaaaggaa cttgttccag gctcagtgc cctcaacacc cccgtcgccg 1260
aaattgagca gtcggcater ggctgtacag tacgatgggc ctgggggggc gtgttccgaa 1320
gtaaaaagggt gggtgtttcg ttaccgacaa ccttgtatcc caccttgata ttttcaccac 1380
ctctcccgcc cgagaagcaa gcattggctg aaaaatccat cctgggttac tatagcaaga 1440
tagcttctgt atgggacaa cctgtgtggc gogaacaagg cttctcgggc gtccccaat 1500
cgagctgtga ccccatctca ttgcccagag ataccagcat cgaagtccat cggcaatggg 1560
ccattacctg tttcatggtc ggagaccggg gacggaagt gtcccaacag tccaagcagg 1620
tacgacagaa gtctgtctgg aaccaactcc ggcagcccta cgagaacgcc ggggcccaag 1680
tcccagagcc ggccaacgtg ctcgagatcg agtggtcgaa gcagcagtat ttccaaggag 1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact ggggttcggcg ctcagaacgc 1800
cgttcaagggt tgttcatttc gttggaacgg agacgtcttt ggtttggaaa ggttatatgg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtggctagc ctgggtgcag 1920
cagcatag 1928

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&lt;210&gt; 44

&lt;211&gt; 591

&lt;212&gt; PRT

<213> *Rhinocycladiella atrovirens*

&lt;400&gt; 44

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Leu Ala Ser Pro
1 5 10 15
Ala Gly Tyr Ser Tyr Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val
20 25 30
Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro
35 40 45
Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys
50 55 60
Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr
65 70 75 80
Tyr Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly
85 90 95
Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val
100 105 110
Pro Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala
115 120 125
Thr Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val
130 135 140
Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val
145 150 155 160
Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val
165 170 175
Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Gly Arg Thr Thr Ile Asn
180 185 190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Lys
195 200 205
Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr Gly
210 215 220
Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro Tyr
225 230 235 240
Gly Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu Leu Leu
245 250 255
Pro Ala Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp Pro Lys Ala
260 265 270
Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala His Tyr Cys
275 280 285
Glu Lys Leu Asn Leu Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg

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      290              295              300
Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser Met Phe Phe Leu Thr
305              310              315              320
Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn Ile Val Ser Asp Lys
      325              330              335
Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Leu
      340              345              350
Cys His Ala Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn
      355              360              365
Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg
      370              375              380
Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys Val Val Leu Pro Thr
      385              390              395              400
Leu Tyr Pro Thr Leu Ile Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
      405              410              415
Ala Leu Ala Glu Lys Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
      420              425              430
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
      435              440              445
Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Glu
      450              455              460
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
      465              470              475              480
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
      485              490              495
Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
      500              505              510
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
      515              520              525
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly
      530              535              540
Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu
      545              550              555              560
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
      565              570              575
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
      580              585              590

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<210> 45
<211> 1928
<212> DNA
<213> Rhinocycladiella atrovirens

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<220>
<221> intron
<222> (739)...(811)

<221> intron
<222> (1134)...(1185)

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gacgcttcgg ccgtgacaga cctgcctac gagaaacagg ttgcccagc attcggcaac      180
ctgcgagctt gtcttgctgc agttggagcc acttcaaacg acattaccac gctcaattac      240
tacatcgtcg actacaaccc gagcaaacct accgcaattg gagatgggct gaaggctacc      300
tttgcccttg ataggctccc tcttgcaag ctggtgccag tgcgggccc ggttcacct      360
gaataacctt ctgagggtga tgctacggcg ctggttcag gacactcaac ccagacaa      420

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gttgoggagc tgggtcgtgtt gggcgctggc ttgagcggtt tggagacggc acgcaaagtc 480
caggctgcgc ggtgtgtctg cctcgtttctt gaggcgatgg atcgtgtggg gggaaagact 540
ctgagcgtac aatcgggtcc cggcaggacg actatcaatg acctcggcgc tgcgtggatc 600
aatgacagca accaaagcga agtattcaaa ttatttgaaa gatttcattt ggagggcgag 660
ctccagagga cgaccgggaa ttcaatccat caagcacaag acggtacaac cactacagct 720
ccttatgggtg attccctgtt aggcacaatt ccatcttgtg atgagacctc tgtcgtgtgt 780
agaatacagt cgtgactcc acatcgtcca gctgagcgag saggttgcaa gtgcactcgc 840
ggaactccct cccgcgtgtt ctcagctgat cgaagagcat agtcttgaag accccaaggc 900
gagccctcaa gcgaagcagc tcgacagtgt gagcttcgca cactactgtg agaaggatct 960
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agccacagag atcagcatgc tttttctcac cgactacatc aagagtgcga ccggtctcag 1080
taatatgttc tcggataaga aagacgggtg gcagtatatg cgatgcaaaa caggtgcgtg 1140
tggtgtcttc tcagtgggag actcgtttct tagtggctat tccaggtatg cagtgcgttt 1200
gccatgccat gtcaaaaggaa cttgttccag gctcagtgca cctcaacacc cccgtcgcg 1260
aaattgagca gtccgcatcc ggtgttacag tacgatcggc ctcgggcggc gtgttccgaa 1320
gtaaaaaggt ggtggtttcg ttaccgacaa ccttgtatcc cacttgata ttttcaccac 1380
ctcttccgcg cgagaagcaa gcattggctg aaaaatccat cctgggctac tatagcaaga 1440
tatcttcgt atgggacaag ctgtgtgtgg gcgaacaagg ctctcgggc gtctccaat 1500
cgagctgtga ccccatctca tttgccagag ataccagcat cgaagtogat cggcaatggt 1560
ccattacctg tttcauggtc ggagaccgga gacggaagtg gtcccaacag tccaagcagg 1620
tacgacagaa gtctgttcgg aaccaactcc ggcgagccta cgagaacgcc ggggcccag 1680
tcccagagcc ggccaacgtg ctccagatcg agtggctgaa gcagcagtat tccaaggag 1740
cgccgagcgc cgtctatggg ctgaactgtc tcaacacact gggttcggcg ctccagaacgc 1800
cgttcaagggt tgttcatttc gttggaacgg agacgtcttt ggtttggaaa gggtatatgg 1860
aaggggccat acgatcgggt cagcgaggcg ctgcagaagt tgtgcctagc ctggtgccag 1920
cagcatag

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&lt;210&gt; 46

&lt;211&gt; 591

&lt;212&gt; PRT

<213> *Rhinocladia atrovirens*

&lt;400&gt; 46

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Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Ala Ser Pro Ala
1      5      10      15
Gly Tyr Ser His Val Gly Val Gly Pro Asn Gly Gly Arg Tyr Val Thr
20      25      30
Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Ala Val Thr Asp Pro Ala
35      40      45
Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys Leu
50      55      60
Ala Ala Val Gly Ala Thr Ser Asn Asp Ile Thr Lys Leu Asn Tyr Tyr
65      70      75      80
Ile Val Asp Tyr Asn Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly Leu
85      90      95
Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val Pro
100     105     110
Val Pro Ala Leu Ala Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala Thr
115     120     125
Ala Leu Val Pro Gly His Ser Thr Pro Asp Asn Val Ala Asp Val Val
130     135     140
Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val Gln
145     150     155     160
Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val Gly
165     170     175
Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile Asn
180     185     190
Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val Phe

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195 200 205  
 Lys Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr Thr  
 210 215 220  
 Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala Pro  
 225 230 235 240  
 Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala Glu  
 245 250 255  
 Leu Leu Pro Ala Trp Ser Gln Leu Ile Glu Glu His Ser Leu Glu Asp  
 260 265 270  
 Pro Lys Ala Ser Pro Gln Ala Lys Gln Leu Asp Ser Val Ser Phe Ala  
 275 280 285  
 His Tyr Cys Glu Lys Asp Leu Asn Leu Pro Ala Val Leu Gly Val Ala  
 290 295 300  
 Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile Ser  
 305 310 315 320  
 Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser Asn  
 325 330 335  
 Ile Val Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys Thr  
 340 345 350  
 Gly Met Gln Ser Leu Cys His Ala Met Ser Lys Glu Leu Val Pro Gly  
 355 360 365  
 Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala Ser  
 370 375 380  
 Gly Cys Thr Val Arg Ser Ala Ser Gly Gly Val Phe Arg Ser Lys Lys  
 385 390 395 400  
 Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Ile Phe Ser Pro Leu  
 405 410 415  
 Pro Ala Glu Lys Gln Ala Leu Ala Glu Lys Ser Ile Gly Tyr Tyr Ser  
 420 425 430  
 Lys Ile Val Phe Val Asp Lys Leu Trp Trp Arg Glu Gln Gly Phe Ser  
 435 440 445  
 Gly Val Leu Gln Ser Ser Cys Asp Pro Ile Ser Phe Ala Arg Asp Thr  
 450 455 460  
 Ser Ile Glu Val Asp Arg Gln Ser Ile Thr Cys Phe Met Val Gly Asp  
 465 470 475 480  
 Pro Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val  
 485 490 495  
 Trp Asn Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro  
 500 505 510  
 Glu Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe  
 515 520 525  
 Gln Ala Pro Ser Ala Val Tyr Gly Leu Asn Cys Leu Asn Thr Leu Gly  
 530 535 540  
 Ser Ala Leu Arg Thr Pro Phe Lys Gly Val His Phe Val Gly Thr Glu  
 545 550 555 560  
 Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 565 570 575  
 Gln Arg Gly Ala Ala Glu Val Val Pro Ser Leu Val Pro Ala Ala  
 580 585 590

<210> 47  
 <211> 600  
 <212> PRT  
 <213> Exophiala spinifera

<400> 47

~~Met Ala Leu Ala Pro Ser Tyr Ile Asn Pro Pro Asn Val Ala Ser Pro~~  
 1 3 10 15

81

Ala Gly Tyr Ser His Val Gly Val Gly Pro Asp Gly Gly Arg Tyr Val  
 20 25 30  
 Thr Ile Ala Gly Gln Ile Gly Gln Asp Ala Ser Gly Val Thr Asp Pro  
 35 40 45  
 Ala Tyr Glu Lys Gln Val Ala Gln Ala Phe Ala Asn Leu Arg Ala Cys  
 50 55 60  
 Leu Ala Ala Val Gly Ala Thr Ser Asn Asp Val Thr Lys Leu Asn Tyr  
 65 70 75 80  
 Tyr Ile Val Asp Tyr Ala Pro Ser Lys Leu Thr Ala Ile Gly Asp Gly  
 85 90 95  
 Leu Lys Ala Thr Phe Ala Leu Asp Arg Leu Pro Pro Cys Thr Leu Val  
 100 105 110  
 Pro Val Ser Ala Leu Ser Ser Pro Glu Tyr Leu Phe Glu Val Asp Ala  
 115 120 125  
 Thr Ala Leu Val Pro Gly His Thr Thr Pro Asp Asn Val Ala Asp Val  
 130 135 140  
 Val Val Val Gly Ala Gly Leu Ser Gly Leu Glu Thr Ala Arg Lys Val  
 145 150 155 160  
 Gln Ala Ala Gly Leu Ser Cys Leu Val Leu Glu Ala Met Asp Arg Val  
 165 170 175  
 Gly Gly Lys Thr Leu Ser Val Gln Ser Gly Pro Gly Arg Thr Thr Ile  
 180 185 190  
 Asn Asp Leu Gly Ala Ala Trp Ile Asn Asp Ser Asn Gln Ser Glu Val  
 195 200 205  
 Ser Arg Leu Phe Glu Arg Phe His Leu Glu Gly Glu Leu Gln Arg Thr  
 210 215 220  
 Thr Gly Asn Ser Ile His Gln Ala Gln Asp Gly Thr Thr Thr Thr Ala  
 225 230 235 240  
 Pro Tyr Gly Asp Ser Leu Leu Ser Glu Glu Val Ala Ser Ala Leu Ala  
 245 250 255  
 Glu Leu Leu Pro Val Trp Ser Gln Leu Ile Glu Glu His Ser Leu Gln  
 260 265 270  
 Asp Leu Lys Ala Ser Pro Gln Ala Lys Arg Leu Asp Ser Val Ser Phe  
 275 280 285  
 Ala His Tyr Cys Glu Lys Glu Leu Asn Leu Pro Ala Val Leu Gly Val  
 290 295 300  
 Ala Asn Gln Ile Thr Arg Ala Leu Leu Gly Val Glu Ala His Glu Ile  
 305 310 315 320  
 Ser Met Leu Phe Leu Thr Asp Tyr Ile Lys Ser Ala Thr Gly Leu Ser  
 325 330 335  
 Asn Ile Phe Ser Asp Lys Lys Asp Gly Gly Gln Tyr Met Arg Cys Lys  
 340 345 350  
 Thr Gly Met Gln Ser Ile Cys His Ala Met Ser Lys Glu Leu Val Pro  
 355 360 365  
 Gly Ser Val His Leu Asn Thr Pro Val Ala Glu Ile Glu Gln Ser Ala  
 370 375 380  
 Ser Gly Cys Thr Val Arg Ser Ala Ser Gly Ala Val Phe Arg Ser Lys  
 385 390 395 400  
 Lys Val Val Val Ser Leu Pro Thr Thr Leu Tyr Pro Thr Leu Thr Phe  
 405 410 415  
 Ser Pro Pro Leu Pro Ala Glu Lys Gln Ala Leu Ala Glu Asn Ser Ile  
 420 425 430  
 Leu Gly Tyr Ser Lys Ile Val Phe Val Trp Asp Lys Pro Trp Trp  
 435 440 445  
 Arg Glu Gln Gly Phe Ser Gly Val Leu Gln Ser Ser Cys Asp Pro Ile  
 450 455 460  
 Ser Phe Ala Arg Asp Thr Ser Ile Asp Val Asp Arg Gln Trp Ser Ile  
 465 470 475 480

```

Thr Cys Phe Met Val Gly Asp Pro Gly Arg Lys Trp Ser Gln Gln Ser
      485      490      495
Lys Gln Val Arg Gln Lys Ser Val Trp Asp Gln Leu Arg Ala Ala Tyr
      500      505      510
Glu Asn Ala Gly Ala Gln Val Pro Glu Pro Ala Asn Val Leu Glu Ile
      515      520      525
Glu Trp Ser Lys Gln Gln Tyr Phe Gln Gly Ala Pro Ser Ala Val Tyr
      530      535      540
Gly Leu Asn Asp Leu Ile Thr Leu Gly Ser Ala Leu Arg Thr Pro Phe
545      550      555      560
Lys Ser Val His Phe Val Gly Thr Glu Thr Ser Leu Val Trp Lys Gly
      565      570      575
Tyr Met Glu Gly Ala Ile Arg Ser Gly Gln Arg Gly Ala Ala Glu Val
      580      585      590
Val Ala Ser Leu Val Pro Ala Ala
      595      600

```

```

<210> 48
<211> 1392
<212> DNA
<213> Unknown

```

```

<220>
<221> CDS
<222> (1)...(1392)

```

```

<223> Cys (-) APAO; removal of cysteine 461

```

```

<400> 48
aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gcc ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
  1          5          10          15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg tcc tgc ctc gtt      96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
          20          25          30

ctt gag gcg atg gat cgt gta ggg gga aag acc ctg agc gta caa tgg      144
Leu Glu Ala Met Asp Arg Val Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45

ggt ccc ggc agg acg act atc aac gac ctc ggc gcc gcg tgg atc aat      192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50          55          60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg      240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
          65          70          75          80

gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa      288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag      336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100          105          110

gag gtt gca agt gca ctt gcg gaa ctc ctc ccc gta tgg cct cag ctg      384
          83

```

Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu	
115 120 125	
atc gaa gag cat agc ctt caa gac ctc aag gcg agc cct cag gcg aag	432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys	
130 135 140	
cgg ctc gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac	480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn	
145 150 155 160	
ttg cct gct gtt ctc gcc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggc gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac gcc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tgc cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala	
210 215 220	
atg tca aag gaa ctt gtt cca gcc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc gcc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa gcc ttc tcg gcc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Gln Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	

```

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
      355                      360                      365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
      370                      375                      380

ccg gcc aac gtg ctc gaa atc gag tgg tgg aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
      385                      390                      395                      400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
      405                      410                      415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
      420                      425                      430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1346
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
      435                      440                      445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
      450                      455                      460

```

&lt;210&gt; 49

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Unknown

&lt;220&gt;

&lt;223&gt; Cys (-) APAO; removal of cysteine 461

&lt;400&gt; 49

```

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1          5          10          15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val
      20          25          30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
      35          40          45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
      50          55          60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
      65          70          75          80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
      85          90          95
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
      100          105          110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
      115          120          125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
      130          135          140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
      85

```

```

145          150          155          160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
          165          170          175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
          180          185          190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
          195          200          205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Cys His Ala
          210          215          220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
          225          230          235          240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
          245          250          255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
          260          265          270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
          275          280          285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
          290          295          300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
          305          310          315          320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
          355          360          365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
          385          390          395          400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

```

&lt;210&gt; 50

&lt;211&gt; 1392

&lt;212&gt; DNA

&lt;213&gt; Unknown

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (1)...(1392)

&lt;223&gt; Cys (-) APAO; removal of cysteines 359 and 461

&lt;400&gt; 50

```

aaa gac aac gtt gcg gac ggg gta ggg ggg ggc gct ggc ttg agc ggt      48
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5          10          15

```

```

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt cag tcc tgc ctc gtc      -96
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val

```

86

	20	25	30	
ctt gag ggc atg gat cgt gta ggg gga aag act ctg agc gta caa tcg				144
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser				
	35	40	45	
ggt ccc ggc agg acg act atc aac gac ctc ggc gct gcg tgg atc aat				192
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn				
	50	55	60	
gac agc aac caa agc gaa gta tcc aga ttg ttc gaa aga ttt cat ttg				240
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu				
	55	70	75	80
gag ggc gag ctc cag agg acg act gga aat tca atc cat caa gca caa				288
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln				
	85	90	95	
gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag				336
Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu				
	100	105	110	
gag gtt gca agt gca ctt ggc gaa ctc ctc ccc gta tgg tct cag ctg				384
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu				
	115	120	125	
atc gaa gag cat agc ctt caa gac ctc aag ggc agc cct cag gcg aag				432
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys				
	130	135	140	
cgg ctc gac agt gtg agc ttc ggc cac tac tgt gag aag gaa cta aac				480
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn				
	145	150	155	160
ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc				528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu				
	165	170	175	
ggt gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc				576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile				
	180	185	190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc				624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly				
	195	200	205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc				672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala				
	210	215	220	
atg tca aag gaa ctt gtt cca ggc tca gtg cac ctc aac acc ccc gtc				720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val				
	225	230	235	240
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg				768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser				
	245	250	255	

```

ggc gcc gtg ttc cga agc aaa aag gtg gtg gtt tgc tta ccg aca acc      815
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
                260                265                270

ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa      864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
                275                280                285

gca ttg ccg gaa aat tct atc ctg gcc tac tat agc aag ata gtc ttc      912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
                290                295                300

gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tgc gcc gtc ctc      960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
                305                310                315                320

caa tgc agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac      1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
                325                330                335

gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga      1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
                340                345                350

cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg      1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp
                355                360                365

gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag      1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
                370                375                380

ccg gcc aac gtg ctc gaa atc gag tgg tgc aag cag cag tat ttc caa      1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
                385                390                395                400

gga gct ccg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
                405                410                415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acg gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
                420                425                430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tgc ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
                435                440                445

caa cga ggt gct gca gaa gtt gtg gct agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
                450                455                460

```

&lt;210&gt; 51

&lt;211&gt; 463

&lt;212&gt; PRT

&lt;213&gt; Unknown



&lt;220&gt;

&lt;223&gt; Cys (-) APAO; removal of cysteines 359 and 461

&lt;400&gt; 51

Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Cys Leu Val  
 20 25 30  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140  
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 145 150 155 160  
 Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu  
 165 170 175  
 Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile  
 180 185 190  
 Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly  
 195 200 205  
 Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala  
 210 215 220  
 Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val  
 225 230 235 240  
 Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser  
 245 250 255  
 Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr  
 260 265 270  
 Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln  
 275 280 285  
 Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe  
 290 295 300  
 Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu  
 305 310 315 320  
 Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp  
 325 330 335  
 Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly  
 340 345 350  
 Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp  
 355 360 365  
 Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu  
 370 375 380  
 Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln  
 385 390 395 400  
 Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly  
 405 410 415  
 Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu  
 420 425 430

Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly  
 435 440 445  
 Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala  
 450 455 460

<210> 52  
 <211> 1392  
 <212> DNA  
 <213> Unknown

<220>  
 <221> CDS  
 <222> (1)...(1392)

<223> Cys (-) APAO; removal of cysteines 169, 359, and  
 461

<400> 52

aaa gac aac gtt gcg gac gtg gta gtg gtg ggc gct ggc ttg agc ggt 48  
 Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly  
 1 5 10 15

ttg gag acg gca cgc aaa gtc cag gcc gcc ggt ctg agc tcc ctg gtt 96  
 Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val  
 20 25 30

ctt gag gcg atg gat cgt gta ggg gga aag act ctg agc gta caa tcc 144  
 Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser  
 35 40 45

ggt ccc ggc agg acg act atc aac gac ctg gcc gct gcg tgg atc aat 192  
 Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn  
 50 55 60

gac agc aac caa agc gaa gta tcc aga ttg ttt gaa aga ttt cat ttg 240  
 Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu  
 65 70 75 80

gag ggc gag ctg cag agg acg act gga aat tca atc cat caa gca caa 288  
 Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln  
 85 90 95

gac ggt aca acc act aca gct cct tat ggt gac tcc ttg ctg agc gag 336  
 Asp Gly Thr Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu  
 100 105 110

gag gtt gca agt gca ctt gcg gaa ctg ctg ccc gta tgg tct cag ctg 384  
 Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu  
 115 120 125

atc gaa gag cat agc ctt caa gat ctg aag gcg agc cct cag gcg aag 432  
 Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys  
 130 135 140

cgg ctg gac agt gtg agc ttc gcg cac tac tgt gag aag gaa cta aac 480  
 Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn  
 145 150 155 160

ttg cct gct gtt ctc ggc gta gca aac cag atc aca cgc gct ctg ctc	528
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu	
165 170 175	
ggg gtg gaa gcc cac gag atc agc atg ctt ttt ctc acc gac tac atc	576
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile	
180 185 190	
aag agt gcc acc ggt ctc agt aat att ttc tcg gac aag aaa gac ggc	624
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly	
195 200 205	
ggg cag tat atg cga tgc aaa aca ggt atg cag tcg att tcg cat gcc	672
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala	
210 215 220	
atg tca aag gaa ctt gtc cca ggc tca gtg cac ctc aac acc ccc gtc	720
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val	
225 230 235 240	
gct gaa att gag cag tcg gca tcc ggc tgt aca gta cga tcg gcc tcg	768
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser	
245 250 255	
ggc gcc gtg ttc cga agc aaa aag gtg gtg gtc tcg tta ccg aca acc	816
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr	
260 265 270	
ttg tat ccc acc ttg aca ttt tca cca cct ctt ccc gcc gag aag caa	864
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln	
275 280 285	
gca ttg gcg gaa aat tct atc ctg ggc tac tat agc aag ata gtc ttc	912
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe	
290 295 300	
gta tgg gac aag ccg tgg tgg cgc gaa caa ggc ttc tcg ggc gtc ctc	960
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu	
305 310 315 320	
caa tcg agc tcc gac ccc atc tca ttt gcc aga gat acc agc atc gac	1008
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp	
325 330 335	
gtc gat cga caa tgg tcc att acc tgt ttc atg gtc gga gac ccg gga	1056
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly	
340 345 350	
cgg aag tgg tcc caa cag tcc aag cag gta cga caa aag tct gtc tgg	1104
Arg Lys Trp Ser Gln Gln Ser Lys Gln Val Arg Gln Lys Ser Val Trp	
355 360 365	
gac caa ctc cgc gca gcc tac gag aac gcc ggg gcc caa gtc cca gag	1152
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu	
370 375 380	
ccg gcc aac gtg ctc gaa atc gag tgg tcg aag cag cag tat ttc caa	1200
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln	

```

385          390          395          400
gga gcc cgg agc gcc gtc tat ggg ctg aac gat ctc atc aca ctg ggt      1248
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415

tcg gcg ctc aga acg ccg ttc aag agt gtt cat ttc gtt gga acc gag      1296
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430

acg tct tta gtt tgg aaa ggg tat atg gaa ggg gcc ata cga tcg ggt      1344
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445

caa cga ggt gct gca gaa gtt gtg gcc agc ctg gtg cca gca gca tag      1392
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala *
          450          455          460

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<210> 53  
 <211> 463  
 <212> PRT  
 <213> Unknown

<220>  
 <223> Cys (-) APAO; removal of cysteines 169, 359, and  
 461

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<400> 53
Lys Asp Asn Val Ala Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
 1          5          10          15
Leu Glu Thr Ala Arg Lys Val Gln Ala Ala Gly Leu Ser Ser Leu Val
          20          25          30
Leu Glu Ala Met Asp Arg Val Gly Gly Lys Thr Leu Ser Val Gln Ser
          35          40          45
Gly Pro Gly Arg Thr Thr Ile Asn Asp Leu Gly Ala Ala Trp Ile Asn
          50          55          60
Asp Ser Asn Gln Ser Glu Val Ser Arg Leu Phe Glu Arg Phe His Leu
          65          70          75          80
Glu Gly Glu Leu Gln Arg Thr Thr Gly Asn Ser Ile His Gln Ala Gln
          85          90          95
Asp Gly Thr Thr Thr Ala Pro Tyr Gly Asp Ser Leu Leu Ser Glu
          100          105          110
Glu Val Ala Ser Ala Leu Ala Glu Leu Leu Pro Val Trp Ser Gln Leu
          115          120          125
Ile Glu Glu His Ser Leu Gln Asp Leu Lys Ala Ser Pro Gln Ala Lys
          130          135          140
Arg Leu Asp Ser Val Ser Phe Ala His Tyr Cys Glu Lys Glu Leu Asn
          145          150          155          160
Leu Pro Ala Val Leu Gly Val Ala Asn Gln Ile Thr Arg Ala Leu Leu
          165          170          175
Gly Val Glu Ala His Glu Ile Ser Met Leu Phe Leu Thr Asp Tyr Ile
          180          185          190
Lys Ser Ala Thr Gly Leu Ser Asn Ile Phe Ser Asp Lys Lys Asp Gly
          195          200          205
Gly Gln Tyr Met Arg Cys Lys Thr Gly Met Gln Ser Ile Ser His Ala
          210          215          220
Met Ser Lys Glu Leu Val Pro Gly Ser Val His Leu Asn Thr Pro Val
          92

```

```

225          230          235          240
Ala Glu Ile Glu Gln Ser Ala Ser Gly Cys Thr Val Arg Ser Ala Ser
          245          250          255
Gly Ala Val Phe Arg Ser Lys Lys Val Val Val Ser Leu Pro Thr Thr
          260          265          270
Leu Tyr Pro Thr Leu Thr Phe Ser Pro Pro Leu Pro Ala Glu Lys Gln
          275          280          285
Ala Leu Ala Glu Asn Ser Ile Leu Gly Tyr Tyr Ser Lys Ile Val Phe
          290          295          300
Val Trp Asp Lys Pro Trp Trp Arg Glu Gln Gly Phe Ser Gly Val Leu
305          310          315          320
Gln Ser Ser Ser Asp Pro Ile Ser Phe Ala Arg Asp Thr Ser Ile Asp
          325          330          335
Val Asp Arg Gln Trp Ser Ile Thr Cys Phe Met Val Gly Asp Pro Gly
          340          345          350
Arg Lys Trp Ser Gln Gln Ser Lys Lys Val Arg Gln Lys Ser Val Trp
          355          360          365
Asp Gln Leu Arg Ala Ala Tyr Glu Asn Ala Gly Ala Gln Val Pro Glu
          370          375          380
Pro Ala Asn Val Leu Glu Ile Glu Trp Ser Lys Gln Gln Tyr Phe Gln
385          390          395          400
Gly Ala Pro Ser Ala Val Tyr Gly Leu Asn Asp Leu Ile Thr Leu Gly
          405          410          415
Ser Ala Leu Arg Thr Pro Phe Lys Ser Val His Phe Val Gly Thr Glu
          420          425          430
Thr Ser Leu Val Trp Lys Gly Tyr Met Glu Gly Ala Ile Arg Ser Gly
          435          440          445
Gln Arg Gly Ala Ala Glu Val Val Ala Ser Leu Val Pro Ala Ala
          450          455          460

```

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<210> 54
<211> 8
<212> PRT
<213> Unknown

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<220>
<223> Artificial Sequence

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<400> 54

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Gly Gly Gly Ser Gly Gly Gly Ser
1          5

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<210> 55
<211> 11
<212> PRT
<213> Exophilal spinifera

```

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<400> 55

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Asp Val Val Val Val Gly Ala Gly Leu Ser Gly
1          5          10

```